

XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.
XX Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;
PI Oestman A, Heldin C, Betscholz C;
XX WPI; 2000-292954/25.
DR N-PSDB; AAA12524.
XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT differentiation, growth and motility of cells expressing the PDGF-C
PT receptor -
XX Disclosure; Fig 4; 135pp; English.
XX The present sequence represents a human platelet-derived growth factor C
CC (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have
CC the ability to stimulate and enhance proliferation or differentiation,
CC and/or growth or motility of cells expressing a PDGF-C receptor.
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
CC proliferation, preferably in combination with one other growth factor
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
CC be used for stimulating connective tissue or wound healing. The
CC PDGF-C polypeptide can be enzymatically processed to generate the active
CC truncated form of PDGF-C and used to regulate the receptor-binding
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC and erythroleukemia, can be identified by testing for expression of
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
CC remodelling during invasion of tumour cells into a normal population of
CC cells. Antagonists can also be used to treat fibrotic conditions,
XX especially found in the lung, kidney or liver.
XX Sequence 318 AA;

Query Match 100.0%; Score 666; DB 21; Length 318;
Best Local Similarity 100.0%; Pred. No. 5e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFVGRKSRVVDLNLITTEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
Db 199 afvgrksrvvdlnlilteevrlyscprnfsvsireelkrttdtfwpgccllvkrcgnca 258
QY 61 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRGLHKSITDVALEHHECDVCVCRGSTGG 120
Db 259 cclhncnecqvpksvtkkyhevlqlrpkgtvrglhksitdvalhehcedvcvrgstgg 318

RESULT 2
AAB58438
ID AAB58438 standard; Protein; 339 AA.
XX AAB58438;
XX 14-MAR-2001 (first entry)
XX Lung cancer associated polypeptide sequence SEQ ID 776.
XX Human; lung cancer associated protein; neuroprotective; cytostatic;
KW cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antiinfective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease.
XX Homo sapiens.
OS
XX WO200055180-A2.
PN
XX

PD 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05918.
XX
XX 12-MAR-1999; 99US-0124270.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX Ruben SM;
PI WPI; 2000-587514/55.
DR N-PSDB; AAF18314.
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer -
XX Claim 11; Page 1305-1306; 1425pp; English.
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the
CC protein or polynucleotide sequences. The lung cancer associated
CC polynucleotide sequences may be used for detection of lung cancer,
CC chromosome identification, as chromosome markers, and for numerous other
CC diagnostic or research purposes. The proteins may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC peptide AAB58549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
CC sequences.
XX Sequence 339 AA;
XX

Query Match 100.0%; Score 666; DB 21; Length 339;
Best Local Similarity 100.0%; Pred. No. 5.4e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFVGRKSRVVDLNLITTEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
Db 220 afvgrksrvvdlnlilteevrlyscprnfsvsireelkrttdtfwpgccllvkrcgnca 279
QY 61 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRGLHKSITDVALEHHECDVCVCRGSTGG 120
Db 280 cclhncnecqvpksvtkkyhevlqlrpkgtvrglhksitdvalhehcedvcvrgstgg 339

RESULT 3
AAY33679
ID AAY33679 standard; Protein; 345 AA.
XX
XX AAY33679;
XX
XX 11-JAN-2000 (first entry)
XX Human VEGF-E protein.
XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;
KW treatment; cardiovascular disorder; endothelial disorder; therapy;
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
KW angiogenic disorder; age-related macular degeneration; vascular disease;
KW neovascularization; tumor; gene mapping.
XX Homo sapiens.
OS
XX

PN WO9947677-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 10-MAR-1999; 99WO-US05190.
 XX
 PR 17-MAR-1998; 98US-0040220.
 PR 02-NOV-1998; 98US-0184216.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ferrara N, Kuo SS;
 PI
 XX WPI; 1999-580306/49.
 DR N-PSDB; AAZ23691.
 XX
 XX New growth factor polypeptide useful for treating cardiovascular or
 PT endothelial disorders, e.g. cardiac hypertrophy
 XX
 PS Claim 1; Fig 2; 122pp; English.
 XX
 CC This invention describes the isolation of a novel human vascular
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
 CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
 CC therapeutically, especially by expressing encoding polynucleotides, to
 CC treat cardiovascular or endothelial disorders in mammals, especially
 CC humans. It is useful in wound repair and tissue generation and
 CC regeneration, and may especially be used to treat cardiac hypertrophy
 CC It can be combined with a carrier in pharmaceutical compositions, which
 CC can be administered to treat disorders as above. VEGF-E can be used to
 CC screen for antagonists and agonists, and the antagonists administered to
 CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or
 CC age-related macular degeneration. It can be used to generate antibodies,
 CC useful therapeutically as antagonists, as above. The antibodies are also
 CC useful to detect VEGF-E polypeptide, especially to diagnose
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
 CC vascular disease, or neovascularization associated with tumor formation),
 CC by contacting the antibody with a tissue sample and detecting formation
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
 CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders
 CC in mammals, by detecting abnormally high or low VEGF-E gene expression in
 CC tissue samples. They can also be used to diagnose a disease or
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
 CC sample. They may also be used to produce probes useful to detect related
 CC sequences or for gene mapping. This sequence represents the human VEGF-E
 CC protein described in the method of the invention.
 XX
 SQ Sequence 345 AA;

Query Match 100.0%; Score 666; DB 20; Length 345;
 Best Local Similarity 100.0%; Pred. No. 5.5e-62;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFVFGKSRVDNLNLTTEVRLYSCTPRNFSVSIRELKRTDIFWPGCLLVKRCGNCA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 226 afvfgkrsrvdnlnteervlyscptrnfsvsireelkrtidfwpgcilvkrcgnca 285
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 61 CCLHNCNECQVPSKVTKKYHVEVLQRPKTVGRGLHKLSTDALEHHECDVCVRGSGTG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 286 cclhncnecqcvpskvtkkyhvevlqrpktvgrglhksltдавlehhеесdvcvrsgtg 345

RESULT 4
 AAY41766
 ID AAY41766 standard; Protein; 345 AA.
 XX
 AC AAY41766;
 XX
 DT 07-DEC-1999 (first entry)
 XX

DE Human PRO200 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX WO9946281-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 08-MAR-1999; 99WO-US05028.
 XX
 PR 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 20-MAR-1998; 98US-0078939.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 09-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083322.
 PR 28-APR-1998; 98US-0083392.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 30-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0084366.
 PR 06-MAY-1998; 98US-0084414.

PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085373.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX
XX (GETH) GENENTECH INC.
XX
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI; 1999-551358/46.
DR N-PSDB; AAZ34296.
XX
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX
XX Claim 12; Fig 207; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAZ41685 to AAZ41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.

XX Sequence 345 AA;

Query Match 100.0%; Score 666; DB 20; Length 345;
Best Local Similarity 100.0%; Pred. No. 5,5e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFVFGKSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
|||||
Db 226 afvfgkrsrvvdlnllteevrlyscptprnfsvsireelkrttdtfwpgcllvkrcgnc 285
Qy 61 CCLHNCNCCQVPSKVTKKYHEVLQRLPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 120
|||||
Db 286 cclhncnccqvpksvktkyhevlqrlprktgvrghlksitdvalehheecdcvcrgstgg 345

RESULT 5
AAV30023

ID AAV30023 standard; Protein; 345 AA.
XX
AC AAV30023;
XX
XX
DT 11-OCT-1999 (first entry)
XX
XX Human vascular endothelial growth factor related protein.
XX Vascular endothelial growth factor related protein; VEGF-R protein;
KW tissue growth inhibition; tumour growth; cancer; tissue growth;
KW angiogenesis; coronary artery blockage.
XX
OS Homo sapiens.
XX
XX WO9937671-A1.
PN
XX
PD 29-JUL-1999.
XX
XX 26-JAN-1999; 99WO-US01574.
PF
XX 31-AUG-1998; 98US-0098548.
PR 27-JAN-1998; 98US-0072635.
PR 05-JUN-1998; 98US-0088089.
PR 24-JUN-1998; 98US-0090544.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX
PI Dou S, Na S, Song HY;
XX
XX WPI; 1999-458680/38.
DR N-PSDB; AAX86352.
XX
XX A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding
PT compounds
XX
XX
PS Claim 1; Page 56-58; 62pp; English.
XX
XX The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC compounds that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue
CC growth, angiogenesis and to treat coronary artery blockage. The
CC VEGF-R coding sequence can be used for the recombinant production of
CC the VEGF-R protein.
XX
XX Sequence 345 AA;

Query Match 100.0%; Score 666; DB 20; Length 345;
Best Local Similarity 100.0%; Pred. No. 5,5e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFVFGKSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
|||||
Db 226 afvfgkrsrvvdlnllteevrlyscptprnfsvsireelkrttdtfwpgcllvkrcgnc 285
Qy 61 CCLHNCNCCQVPSKVTKKYHEVLQRLPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 120
|||||
Db 286 cclhncnccqvpksvktkyhevlqrlprktgvrghlksitdvalehheecdcvcrgstgg 345

RESULT 6
AAB48657
ID AAB48657 standard; Protein; 345 AA.
XX
AC AAB48657;
XX
XX 09-MAR-2001 (first entry)
XX
XX Human zvegfg3, SEQ ID NO:33.

XX Human; zvegfg3; zvegfg4 fusion; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
KW immunomodulation; hepatic.
XX Homo sapiens.
XX WO200066736-A1.
XX 09-NOV-2000.
XX 03-MAY-2000; 2000WO-US40047.
XX 03-MAY-1999; 99US-0304216.
XX 10-NOV-1999; 99US-0164463.
XX 04-FEB-2000; 2000US-0180169.
XX (2YMO) ZYMOGENETICS INC.
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX WPI; 2000-687541/67.
XX N-PSDB; AAC81582.
XX Growth factor homologs and the nucleic acids that encode them, useful
XX e.g. for treating liver damage, ischemia, multiple sclerosis and
XX Alzheimer's disease -
XX Claim 48; Page 125-126; 143pp; English.
XX The invention relates to the human growth factor homologue zvegfg4
XX (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member
XX of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
XX growth factor) family. Zvegfg4 has a growth factor domain (AAB48654)
XX characterised by a PDGF cysteine knot structure, and a CUB domain
XX (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like
XX activity, having mitogenic activity on fibroblasts, vascular smooth
XX muscle cells and pericytes, and has also been shown to stimulate bone
XX growth. The invention also relates to fusion proteins comprising human
XX zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3
XX fusions; expression constructs and host cells comprising human zvegfg4
XX nucleic acids; the recombinant expression of human zvegfg4; an antibody
XX which binds to human zvegfg4 or a fragment thereof; a method of activating
XX a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a
XX method of modulating the proliferation, differentiation, migration or
XX metabolism of bone cells, comprising exposing bone cells to
XX zvegfg4-derived polypeptides; and a method of detecting a genetic
XX abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived
XX fragments may be used to stimulate tissue development or repair, or
XX cellular differentiation or proliferation. They are particularly used for
XX the treatment or repair of liver damage, and may also be used to
XX modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
XX multiple sclerosis). Due to their osteogenic activity, they may be used
XX in the treatment of periodontal disease and fractures. They may also be
XX used to enhance expansion and mobilisation of haematopoietic stem cells
XX and endothelial precursor stem cells, which may be useful in the
XX treatment of ischaemia, in wound healing, and in the modulation of the
XX immune system. The present sequence represents human zvegfg3.
XX Sequence 345 AA;
XX Query Match 100.0%; Score 666; DB 21; Length 345;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-62;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 AFVFGKSRVVDNLNLTVEVRLYSCPTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCA 60
XX |
XX 226 afvfgkrrvvdnlntteevrlyscptprnfsvsireelkrttdtlfwpgcllvkrcgncgca 285

QY 61 CCLHNCNECCVPSKVTKYKHYEVQLQRPKTVGRGLHKSLSLTDVALEHHECCDCVCRGSGTG 120
Db 286 cclhncnecqcvpskvtkkyheviqlrpkrtgvrghksltvdalehheccdcvcrsgtgg 345
RESULT 7
AAB24250
ID AAB24250 standard; Protein; 345 AA.
XX AC AAB24250;
XX DT 08-FEB-2001 (first entry)
XX DE Human platelet-derived growth factor related protein LP8.
XX KW Human; platelet derived growth factor related protein; LP8; VEGFh;
KW vascular endothelial growth factor h; tissue regeneration; vulnery;
KW atherosclerosis; PDGF-related protein; antiarteriosclerotic.
XX OS Homo sapiens.
XX PN WO200059940-A2.
XX PD 12-OCT-2000.
XX PF 24-MAR-2000; 2000WO-US06427.
XX PR 06-APR-1999; 99US-0127913.
XX PA (ELIL) LILLY & CO ELI.
XX PI Hammond LJ, Na S;
XX WPI; 2000-664991/64.
XX N-PSDB; AAC64426.
XX Enhancing tissue growth and promoting wound healing by administering
XX platelet-derived growth factor related protein, LP8 or its analog and
XX treating atherosclerosis by administering LP8 antagonist -
XX Claim 4; Page 63-64; 64pp; English.
XX The present invention describes a method for enhancing tissue growth,
XX promoting wound healing or stimulating smooth muscle growth by
XX administering a platelet-derived growth factor (PDGF) related protein,
XX designated LP8 or its analogue. Also described is a method of slowing
XX the progress of atherosclerosis or treating atherosclerosis comprising
XX the administration of an LP8 antagonist. The method is useful for
XX enhancing tissue growth, promoting wound healing and stimulating smooth
XX muscle growth. Antagonists of LP8 are useful for treating
XX atherosclerosis. The present sequence represents human LP8, which is
XX also called VEGFh.
XX Sequence 345 AA;
XX Query Match 100.0%; Score 666; DB 21; Length 345;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-62;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 AFVFGKSRVVDNLNLTVEVRLYSCPTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGNCA 60
XX |
XX 226 afvfgkrrvvdnlntteevrlyscptprnfsvsireelkrttdtlfwpgcllvkrcgncgca 285
QY 61 CCLHNCNECCVPSKVTKYKHYEVQLQRPKTVGRGLHKSLSLTDVALEHHECCDCVCRGSGTG 120
Db 286 cclhncnecqcvpskvtkkyheviqlrpkrtgvrghksltvdalehheccdcvcrsgtgg 345
RESULT 8
AAB44322
ID AAB44322 standard; Protein; 345 AA.
XX

AC AAB44322;
XX 08-FEB-2001 (first entry)
XX Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
XX Human; secreted protein; transmembrane protein; PRO; EST; cytotstatic;
KW expressed sequence tag; detection; cancer.
XX Homo sapiens.
XX WO200053756-A2.
XX 14-SEP-2000.
XX 18-FEB-2000; 2000WO-US04341.
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 29-MAR-1999; 99US-0126773.
XX 21-APR-1999; 99US-0130232.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 23-JUN-1999; 99US-0141037.
XX 26-JUL-1999; 99US-0145698.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28565.
XX 16-DEC-1999; 99WO-US30095.
XX 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kiljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI: 2000-611443/58.
XX N-PSDB: AAC78582.
XX Novel PRO polypeptides and polynucleotides used in detection methods,
XX to target bioactive molecules to specific cells, and to modulate
XX cellular activities -
XX Claim 12; Fig 207; 636pp; English.
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
XX sequence tag) sequences which encode secreted or transmembrane PRO
XX polypeptides. The PRO polynucleotides and polypeptides have cytostatic
XX activity. The polynucleotides and polypeptides can be used for detecting
XX the presence of PRO polypeptides in samples, for linking bioactive
XX molecules to cells and for modulating biological activities of cells,
XX using the polypeptides for specific targeting. The polypeptide targeting
XX can be used to kill the target cells, e.g. for the treatment of cancers.
XX The polypeptide pairs provide specific targeting of bioactive molecules
XX to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
XX the isolation of the PRO polynucleotide sequences.
XX Sequence 345 AA;
XX
XX Query Match 100.0%; Score 666; DB 21; Length 345;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-62;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AFVGRKSRVVDNLLTTEVRLYCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCA 60
XX
XX Db 226 afvgrksrvvdnlntteevrlyscprnfsvsireelkrttdtlfwpgcllvkrcgnca 285
XX
XX Qy 61 CCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGHHKSLTDVALEHHEECDCVCRGSGG 120
XX
XX Db 286 cclhncnecqvpstkvtkkyhevlqlrpkgtgvrghksltvalenheecdcvcrgstgg 345
XX
XX RESULT 9
XX AAB10633
XX ID AAB10633 standard; Protein; 345 AA.
XX AC AAB10633;
XX XX
XX 19-JAN-2001 (first entry)
XX DE Human RACE generated VEGF-X protein.
XX XX
XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX venous sore; diabetic ulcer; burns; skin graft growth.
XX Homo sapiens.
XX OS
XX WO200037641-A2.
XX PN
XX 29-JUN-2000.
XX PD
XX 21-DEC-1999; 99WO-US30503.
XX PF
XX 22-DEC-1998; 98GB-0028377.
XX PR
XX 18-MAR-1999; 99US-0124967.
XX PR
XX 08-NOV-1999; 99US-0164131.
XX XX
XX (JANC) JANSSEN PHARM NV.
XX PA
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX PI
XX WPI: 2000-442669/38.
XX DR
XX N-PSDB: AAA71951.
XX XX
XX New vascular endothelial growth factor protein, useful for treating or
XX preventing diseases associated with inappropriate angiogenesis activity
XX such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 6; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
XX (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
XX (VEGF-X) cytostatic, antirheumatic, antidiabetic, antipsoriatic and
XX antidiabetic activity and acts as an angiogenesis and vascularization
XX regulator. An antisense molecule of the invention is useful for treating
XX or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX retinopathy by inhibiting angiogenic activity or inappropriate
XX vascularization including formation and proliferation of new blood
XX vessels, growth and development of tissues, tissue regeneration and organ
XX and tissue repair in a subject. The products of the invention are useful
XX for preparing medicaments for treating wounds such as dermal ulcers,
XX pressure sores, venous sores, diabetic ulcers and burns and to promote
XX skin graft growth, tissue repair, proliferation of new blood vessels,
XX tissue regeneration and organ repair by promoting angiogenic activity or
XX vascularization. This sequence represents the RACE generated human VEGF-X
XX protein described in the method of the invention.
XX
XX Sequence 345 AA;
XX
XX Query Match 100.0%; Score 666; DB 21; Length 345;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-62;
XX

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFVFGKSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
|||||
Db 226 atvfgkrrvvdnlntteevrlyscprnfsvsireelkrttdtiffpgcllvkrcgnc 285
QY 61 CCLHNCNECQVPSKVTKKYHEVLQLRPKTGVGRGLHSLTDVALEHHBECDCVCRGSGTG 120
|||||
Db 286 cclhncnecqvpkvtkkyhevlqirpktgvrghlsldvalehheecdcvcrgstg 345

RESULT 10
AAB10634
ID AAB10634 standard; Protein; 345 AA.
AC AAB10634;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF-X homologue protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
OS Homo sapiens.
XX
XX WO200037641-A2.
PN
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
XX (JANC) JANSSEN PHARM NV.
PA
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
XX WPI: 2000-442669/38.
DR
DR N-PSDB; AAA71952.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 7; 127pp; English.
PS
XX This invention describes a novel vascular endothelial growth factor-X
XX (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC homologue described in the method of the invention.
XX
XX Sequence 345 AA;

Query Match 100.0%; Score 666; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.5e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFVFGKSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
|||||
Db 226 atvfgkrrvvdnlntteevrlyscprnfsvsireelkrttdtiffpgcllvkrcgnc 285
QY 61 CCLHNCNECQVPSKVTKKYHEVLQLRPKTGVGRGLHSLTDVALEHHBECDCVCRGSGTG 120
|||||
Db 286 cclhncnecqvpkvtkkyhevlqirpktgvrghlsldvalehheecdcvcrgstg 345

RESULT 11
AAB10635
ID AAB10635 standard; Protein; 345 AA.
XX
AC AAB10635;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF-X protein #1 isolated from clones 4 and 7.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
OS Homo sapiens.
XX
XX WO200037641-A2.
PN
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
XX (JANC) JANSSEN PHARM NV.
PA
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
XX WPI: 2000-442669/38.
DR
DR N-PSDB; AAA71955.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 9; 127pp; English.
PS
XX This invention describes a novel vascular endothelial growth factor-X
XX (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC isolated from clones 4 and 7 described in the method of the invention.
CC

XX Sequence 345 AA;
SQ

Query Match 100.0%; Score 666; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.5e-62; Indels 0; Gaps 0;
Matches 120; Conservative 0; Mismatches 0;

Qy 1 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA 60
|||||
Db 226 afvfgkrsvvdnlntteevrlyscprnfsvsireelkrttdtfwpgcllvkrcggnc 285
|||||

Qy 61 CCLHNCNECQVPSKVTYKHYEVLQRPKTGVRGLHKSITDVALEHHEEDCDVCRGSGTG 120
|||||
Db 286 cclhncnecqvpvskvtykkyhevlqlrpkgtgvrghksitdvalenheecdcvrgstgg 345
|||||

RESULT 12
AAB10636
ID AAB10636 standard; Protein; 345 AA.
AC AAB10636;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF-X protein #2 isolated from clones 4 and 7.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytotstatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI; 2000-442669/38.
DR N-PSDB; AAA71955.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Claim 1; Fig 10; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnerary, cytotstatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,

CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC isolated from clones 4 and 7 described in the method of the invention.
XX
SQ Sequence 345 AA;
Query Match 100.0%; Score 666; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.5e-62; Indels 0; Gaps 0;
Matches 120; Conservative 0; Mismatches 0;

Qy 1 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA 60
|||||
Db 226 afvfgkrsvvdnlntteevrlyscprnfsvsireelkrttdtfwpgcllvkrcggnc 285
|||||

Qy 61 CCLHNCNECQVPSKVTYKHYEVLQRPKTGVRGLHKSITDVALEHHEEDCDVCRGSGTG 120
|||||
Db 286 cclhncnecqvpvskvtykkyhevlqlrpkgtgvrghksitdvalenheecdcvrgstgg 345
|||||

RESULT 13
AAB10644
ID AAB10644 standard; Protein; 345 AA.
AC AAB10644;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF-X protein #4.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytotstatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI; 2000-442669/38.
DR N-PSDB; AAA71990.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Disclosure; Fig 30B; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnerary, cytotstatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful

CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents a human VEGF-X protein
 CC described in the method of the invention.

XX Sequence 345 AA;

Query Match 100.0%; Score 666; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 5.5e-62;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AFVGRKSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
 Db 226 afvgrksrvvdnlnteervlyscprnfsvsireelkrtdtifwpgcllvkrcgnca 285
 QY 61 CCLHNCNECQCVPKVKYKHYEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 120
 Db 286 cclhncnecqcvpskvtkkyhyevlqlrpkgtgvrghksltdvalehheecdvcrgstgg 345

RESULT 14

AAB10650
 ID AAB10650 standard; Protein; 345 AA.

XX AAB10650;

XX 19-JAN-2001 (first entry)

DE Human 990126veg protein.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 XX venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure; Fig 11; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation and proliferation of new blood

CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents the human 990126veg protein
 CC used to illustrate the method of the invention.

XX Sequence 345 AA;

Query Match 100.0%; Score 666; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 5.5e-62;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AFVGRKSRVVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
 Db 226 afvgrksrvvdnlnteervlyscprnfsvsireelkrtdtifwpgcllvkrcgnca 285
 QY 61 CCLHNCNECQCVPKVKYKHYEVLQRPKTGVRGLHKSITDVALEHHEECDCVCRGSTGG 120
 Db 286 cclhncnecqcvpskvtkkyhyevlqlrpkgtgvrghksltdvalehheecdvcrgstgg 345

RESULT 15

AAB10651
 ID AAB10651 standard; Protein; 345 AA.

XX AAB10651;

XX 19-JAN-2001 (first entry)

XX Human VEGF-X protein #3.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Claim 72; Fig 12; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC described in the method of the invention.

xx

SQ Sequence 345 AA;

Query Match 100.0%; Score 666; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 5,5e-62;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AFVFGKRSYVDNLNLTTEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
226 afvfgkrsrvdnlalteevrlyscprnfsvsireelkrttdtifwpgcllvkrcgnc 285
QY 61 CCLHNCNEQCQVPSKVTKYHEVLQLRPKTGVRGLHKS LTDVALEHHECDVCVRGSGG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
286 cclhncnecqcvpskvtkyhevqlrpkgtgvrghksltdvalehhecdvcvrgstgg 345

Search completed: January 15, 2002, 22:14:47
Job time: 1809 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2002, 22:14:53 ; Search time 24.08 Seconds
(without alignments)
112.143 Million cell updates/sec

Title: US-09-457-066-2_COPY_226_345
Perfect score: 666
Sequence: 1 AFVFGKRSRVVDLNLITEV.....DVALEHHECDVCGSTGG 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs., 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119.5	17.9	321	4 US-08-915-795-9	Sequence 9, Appli
2	119.5	17.9	358	4 US-08-915-795-8	Sequence 8, Appli
3	115.5	17.3	325	4 US-08-915-795-3	Sequence 3, Appli
4	115.5	17.3	354	4 US-08-915-795-5	Sequence 5, Appli
5	108	16.2	190	3 US-08-867-352-25	Sequence 25, Appl
6	108	16.2	220	6 5175255-4	Patent No. 5175255
7	108	16.2	241	1 US-08-387-845-4	Sequence 4, Appli
8	108	16.2	241	2 US-08-999-811-6	Sequence 6, Appli
9	108	16.2	241	2 US-08-778-275-4	Sequence 4, Appli
10	108	16.2	241	2 US-08-824-996-8	Sequence 8, Appli
11	108	16.2	241	3 US-08-989-251-29	Sequence 29, Appl
12	108	16.2	241	3 US-09-042-105-6	Sequence 6, Appli
13	108	16.2	241	3 US-08-867-352-4	Sequence 4, Appli
14	108	16.2	241	3 US-09-340-250-29	Sequence 29, Appl
15	108	16.2	241	4 US-08-795-430-54	Sequence 54, Appl
16	108	16.2	241	5 PCT-US96-09001-9	Sequence 9, Appli
17	108	16.2	241	6 5194536-15	Patent No. 5194596
18	108	16.2	241	6 5219739-15	Patent No. 5219739
19	107.5	16.1	256	6 5175255-9	Patent No. 5175255
20	105.5	15.8	188	1 US-08-469-427A-11	Sequence 11, Appl
21	105.5	15.8	188	2 US-08-609-443B-11	Sequence 11, Appl
22	105.5	15.8	188	2 US-08-569-063C-11	Sequence 11, Appl
23	105.5	15.8	188	4 US-08-795-430-57	Sequence 57, Appl
24	105.5	15.8	207	2 US-08-609-443B-15	Sequence 15, Appl
25	105.5	15.8	207	2 US-08-569-063C-15	Sequence 15, Appl
26	105	15.8	109	1 US-08-094-079-2	Sequence 2, Appli
27	105	15.8	109	1 US-08-094-079-3	Sequence 3, Appli

28	105	15.8	109	2 US-08-804-953-3	Sequence 3, Appli
29	105	15.8	109	3 US-08-691-794-4	Sequence 4, Appli
30	105	15.8	109	5 PCT-US91-02766-18	Sequence 18, Appl
31	105	15.8	109	5 PCT-US93-02612-1	Sequence 1, Appli
32	105	15.8	109	6 5498600-3	Patent No. 5498600
33	105	15.8	119	2 US-08-257-494D-1	Sequence 1, Appli
34	105	15.8	120	6 5428135-2	Patent No. 5428135
35	105	15.8	146	3 US-08-989-251-2	Sequence 2, Appli
36	105	15.8	146	3 US-08-989-251-25	Sequence 25, Appl
37	105	15.8	146	3 US-09-340-250-2	Sequence 2, Appli
38	105	15.8	146	3 US-09-340-250-25	Sequence 25, Appl
39	105	15.8	160	1 US-08-094-079-1	Sequence 1, Appli
40	105	15.8	205	3 US-08-989-251-27	Sequence 27, Appl
41	105	15.8	205	3 US-08-989-251-37	Sequence 37, Appl
42	105	15.8	205	3 US-09-340-250-27	Sequence 27, Appl
43	105	15.8	205	3 US-09-340-250-37	Sequence 37, Appl
44	105	15.8	282	1 US-08-445-847A-1	Sequence 1, Appli
45	104.5	15.7	109	3 US-08-691-794-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
US-08-915-795-9

Query Match 17.9%; Score 119.5; DB 4; Length 321;
Best Local Similarity 33.3%; Pred. No. 1.6e-05;
Matches 36; Conservative 15; Mismatches 42; Indels 15; Gaps 6;

RESULT 5
US-08-867-352-25
; Sequence 25, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multicistronic expression units and their use
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,352
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/397,847
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-867-352-25


```
Query Match          16.2%; Score 108; DB 2; Length 241;
Best Local Similarity 34.7%; Pred. No. 0.0002;
```

Query Match 16.2%; Score 108; DB 3; Length 241;
Best Local Similarity 34.7%; Pred. No. 0.0002;

Query Match 16.2%; Score 108; DB 3; Length 241;
Best Local Similarity 34.7%; Pred. No. 0.0002;
Matches 42: Conservative 12; Mismatches 35; Indels 32; Gaps 11;

```

Query Match      16.2%  Score 108;  DB 3;  Length 241;
Best Local Similarity 34.7%;  Pred. No. 0.0002;
Matches 42;  Conservative 12;  Mismatches 35;  Indels 32;  Gaps 11;

QY      5  GRKSRVVDLNLIT--EEVRLYSCTPRN--FSVSIRELKRITDTIF--WPGCLLVKRCGGN  58
      |||  |  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      79  GRRS-----LGSLLTAEPAMIAECKTRTEVEFIS--RRLIDRTNANFLWPPCVCVEQRCSG- 132

QY      59  CACCLHNCNECQVPKVKTKYHEVLQRP-----KTGV--RGLHKLSLTDVALESHHEECD 111
      ||  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      133  --CG--NNRNVCQRTQV-----QLRPQVQVKKIEIVRKKPIFKKAT--VTLEDHLACK 179

QY      112  C 112
      |
Db      180  C 180

RESULT 14
US-09-340-250-29
; Sequence 29, Application US/09340250
; Patent No. 6083723
; GENERAL INFORMATION:
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN YEAST
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh

```

3

Search completed: January 15, 2002, 22:15:41
Job time: 48 sec

OM of: US-09-457-066-2_COPY_226_345 to: GenEmbl:* out_format : pfs

Date: Jan 15, 2002 11:05 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q/cgn2_1/USPTO.spool/US09457066/runat_15012002_132155_14200/app_query.fasta_1.190
-DB=GenEmbl -OFMT=fastap -SUFFIX=rge -CAPOF=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPECL=0.000 -LOOPEXT=0.500 -QGAPOF=4.500
-QGAPEXT=0.050 -XGAPOF=10.000 -XGAPEXT=0.500 -FGAPOF=6.000
-FGAPEXT=7.000 -YGAPOF=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZ=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09457066 @CEN1_1_6066
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-457-066-2_COPY_226_345

Query length: 120

Database: GenEmbl.*

Database sequences: 1472140

Database length: -341344837

Search time (sec): 1337.100000

score_list:

Sequence	Strd	Orig	zScore	EScore	Len	Documentation
gb_pat:AX027935	+	666.00	1279.06	5.7e-63	1035	AX027935 Sequence 3 from Paten
gb_pr:AX028032	+	666.00	1279.06	5.7e-63	1035	AX028032 Sequence 3 from Paten
gb_pat:AX044518	+	666.00	1274.53	1.0e-62	1760	AX044518 Sequence 32 from Paten
gb_pat:AX118785	+	666.00	1274.53	1.0e-62	1760	AX118785 Sequence 1 from Paten
gb_pr:AF260738	+	666.00	1274.32	1.1e-62	1804	AF260738 Homo sapiens platelet
gb_pr:AB033831	+	666.00	1274.26	1.1e-62	1817	AB033831 Homo sapiens hSCDGF m
gb_pr:AF244813	+	666.00	1272.81	1.3e-62	2152	AF244813 Homo sapiens platelet
gb_pat:AX047650	+	666.00	1270.42	1.7e-62	2849	AX047650 Sequence 9 from Paten
gb_pr:AF091434	+	666.00	1269.96	1.8e-62	3007	AF091434 Homo sapiens secretin
gb_ro:AF117608	+	624.00	1189.29	5.7e-58	2692	AF117608 Mus musculus fallotell
gb_ro:AF266467	+	624.00	1187.03	7.7e-58	3512	AF266467 Mus musculus platelet
gb_pat:AX044520	+	624.00	1186.88	7.8e-58	3571	AX044520 Sequence 34 from Paten
gb_pat:AX118787	+	624.00	1186.88	7.8e-58	3571	AX118787 Sequence 3 from Paten
gb_ro:AB033830	+	611.00	1171.54	5.6e-57	1116	AB033830 Rattus norvegicus rsc
gb_ro:AF286725	+	608.00	1166.33	1.1e-56	1038	AF286725 Mus musculus platelet
gb_ov:AB033829	+	585.00	1117.56	5.7e-54	1675	AB033829 Gallus gallus SCDGF m
gb_pat:AX027968	+	513.00	992.94	5.0e-47	279	AX027968 Sequence 36 from Paten
gb_pat:AX027989	+	513.00	992.94	5.0e-47	279	AX027989 Sequence 57 from Paten
gb_sv:AX028055	+	513.00	992.94	5.0e-47	279	AX028055 Sequence 35 from Paten
gb_sv:AX028086	+	513.00	992.94	5.0e-47	279	AX028086 Sequence 57 from Paten
gb_pat:AX027967	+	472.00	913.85	1.3e-42	261	AX027967 Sequence 35 from Paten
gb_pat:AX027988	+	472.00	913.85	1.3e-42	261	AX027988 Sequence 56 from Paten
gb_sv:AX028064	+	472.00	913.85	1.3e-42	261	AX028064 Sequence 55 from Paten
gb_sv:AX028085	+	472.00	913.85	1.3e-42	261	AX028085 Sequence 56 from Paten
em_hlg_hum:AC009582	-	417.00	750.71	1.5e-33	191314	AC009582 Homo sapiens chrom
gb_hlg:AC092608	-	417.00	750.30	1.6e-33	200864	AC092608 Homo sapiens chrom
gb_pat:AX027969	+	390.00	754.48	9.5e-34	262	AX027969 Sequence 37 from Paten
gb_pat:AX027992	+	390.00	754.48	9.5e-34	262	AX027992 Sequence 60 from Paten
gb_sv:AX028066	+	390.00	754.48	9.5e-34	262	AX028066 Sequence 37 from Paten
gb_sv:AX028089	+	390.00	754.48	9.5e-34	262	AX028089 Sequence 60 from Paten
gb_pat:AX027973	+	351.00	679.74	1.4e-29	232	AX027973 Sequence 41 from Paten
gb_pat:AX028002	+	351.00	679.74	1.4e-29	232	AX028002 Sequence 70 from Paten
gb_sv:AX028070	+	351.00	679.74	1.4e-29	232	AX028070 Sequence 41 from Paten
gb_sv:AX028099	+	351.00	679.74	1.4e-29	232	AX028099 Sequence 70 from Paten
gb_hlg:AC015451	+	340.00	608.31	1.3e-25	82113	AC015451 Homo sapiens Clone R
gb_pat:AX164748	+	324.00	613.90	6.4e-26	1113	AX164748 Sequence 5 from Paten
gb_ro:AF335583	+	324.00	613.90	6.4e-26	1113	AF335583 Mus musculus platelet
gb_ro:AB052170	+	324.00	612.03	8.2e-26	1386	AB052170 Rattus norvegicus rsc
gb_pr:AB033832	+	324.00	611.78	8.4e-26	1428	AB033832 Homo sapiens hSCDGF-R
gb_pat:AX044538	+	324.00	611.52	8.7e-26	1472	AX044538 Sequence 52 from Paten

gb_pat:AX164746 + 324.00 610.88 9.5e-26 1587 ! AX164746 Sequence 3 from Pa
gb_pat:AX164744 + 324.00 609.67 1.1e-25 1828 ! AX164744 Sequence 1 from Pa
gb_pr:AF335584 + 324.00 609.67 1.1e-25 1828 ! AF335584 Homo sapiens plate
gb_pat:AX044487 + 324.00 609.42 1.1e-25 1882 ! AX044487 Sequence 1 from Pa
gb_pr:AF336376 + 324.00 607.89 1.4e-25 2253 ! AF336376 Homo sapiens plate

seq_name: gb_pat:AX027935

seq_documentation_block:

LOCUS AX027935 1035 bp DNA PAT 16-SEP-2000
DEFINITION Sequence 3 from Patent WO0037641.
ACCESSION AX027935
VERSION AX027935.1 GI:10188752
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE Vascular endothelial growth factor-x
JOURNAL Patent: WO 0037641-A 3 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSIENA JOHANNA HUBER (BE) ;
JANSSEN PHARMACEUTICA NV (BE) ; SPRENGEL JORG JURGEN (BE) ; YON
JEFFREY ROLAND (BE) ; XU JEAN (US) ; GOSIEWSKA ANNA (US) ; DHANARAJ
SRIDEVI NAIDU (US)
FEATURES Location/Qualifiers
source
1..1035
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 301 a 213 c 251 g 270 t
ORIGIN

alignment_scores:
Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_226_345 x AX027935

Align seg 1/1 to: AX027935 from: 1 to: 1035

1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
676 GCTTTTGTGTTTTGGAAGAAATCCAGAGTGGTGATCTGAACCTTCTAAC 725
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||
726 AGAGGAGGTAAAGTTATACAGCTGCACACTCGTAACCTCTCAGTGCTCA 775
34 leArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeu 50
|||||
776 TAAGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTTGCTC 825
51 LeuValLysArgCysGlyClyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
826 CTGGTTAAACGCTGGTGGGAACCTGCTGCTGTGTCACCAATTCGCA 875
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluVal 84
|||||
876 TGAATGTCAATGTGTCACCAAGAAATGTTACTAAAAATACACGAGGTCC 925
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
926 TTCAGTTGAGACCAAGACCGGTGTCAGGGGATTCACAAATACCTCACC 975
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
|||||
976 GACGTGGCCCTGGACCAACCATGAGGAGTGTGACTGTGTGTCAGAGGGAG 1025

117 rThrGlyGly 120

|||||

1026 CACAGGAGGA 1035

seq_name: gb_pr:AX028032

seq_documentation_block:

LOCUS AX028032 1035 bp DNA

DEFINITION Sequence 3 from Patent WO0037641.

ACCESSION AX028032

VERSION AX028032.1

KEYWORDS AX028032.1 GI:10188844

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1035)

AUTHORS Gordon, R.D., Dijkmans, J.J., Sprengel, J.J., Yon, J.R., Xu, J.,

Gosiewska, A. and Dhanaraj, S.N.

TITLE Vascular endothelial growth factor-x

JOURNAL Patent: WO 0037641-A 29-JUN-2000;

GORDON ROBERT DOUGLAS (BE); DIJKMANS JOSIENA JOHANNA HUBER (BE);

JANSSEN PHARMACEUTICA NV (BE); SPRENGEL JORG JURGEN (BE); YON

JEFFREY ROLAND (BE); XU JEAN (US); GOSIEWSKA ANNA (US); DHANARAJ

SRIDEVI NAIDU (US)

FEATURES

Location/Qualifiers

1..1035

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 301 a 213 c 251 g 270 t

ORIGIN

alignment_scores:

Quality: 666.00 Length: 120

Ratio: 5.550 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_226_345 x AX028032

Align seg 1/1 to: AX028032 from: 1 to: 1035

1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17

676 GCTTTGTTTTGGAGAGAAATCCAGAGTGGTGAATCTGAACCTCTTAAC 725

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34

726 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGCCA 775

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50

776 TAAGGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTGTCTC 825

51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67

826 CTGGTTAAACGTGTGGTGGGAACCTGTGCTGTCTCCACAAATTCGAA 875

67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluVal 84

876 TGAATGTCATTAAGTGTCCCAAGCAAGTTACTAAAAATACACAGAGTCC 925

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100

926 TTCAGTTGAGACCAAGACCGGTGTGAGGGGATTCACAAATCACTCAC 975

101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117

976 GACGTGGCCCTGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAG 1025

117 rThrGlyGly 120

|||||

1026 CACAGGAGGA 1035

seq_name: gb_pat:AX044518

seq_documentation_block:

LOCUS AX044518 1760 bp DNA

DEFINITION Sequence 32 from Patent WO0066736.

ACCESSION AX044518

VERSION AX044518.1

KEYWORDS AX044518.1 GI:11343373

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1760)

AUTHORS Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.

TITLE Growth factor homolog zveg14

JOURNAL Patent: WO 0066736-A 32 09-NOV-2000;

ZymoGenetics, Inc. (US)

FEATURES

Location/Qualifiers

1..1760

/organism="Homo sapiens"

/db_xref="taxon:9606"

154..1191

/note="unnamed protein product"

/codon_start=1

/protein_id="CAC117170.1"

/db_xref="GI:11343374"

BASE COUNT 494 a 373 c 411 g 482 t

ORIGIN

alignment_scores:

Quality: 666.00 Length: 120

Ratio: 5.550 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_226_345 x AX044518

Align seg 1/1 to: AX044518 from: 1 to: 1760

1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17

829 GCTTTGTTTTGGAGAGAAATCCAGAGTGGTGAATCTGAACCTCTTAAC 878

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34

879 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGCCA 928

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50

929 TAAGGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTGTCTC 978

51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67

979 CTGGTTAAACGTGTGGTGGGAACCTGTGCTGTCTCCACAAATTCGAA 1028

67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluVal 84

1029 TGAATGTCATTAAGTGTCCCAAGCAAGTTACTAAAAATACACAGAGTCC 1078

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100

1079 TTCAGTTGAGACCAAGACCGGTGTGAGGGGATTCACAAATCACTCAC 1128

```

101 AspValAlaLeuGluHisGluCysAspCysValCysArgGlySe 117
|||||
1129 GACGTGGCCCTGGAGCACCATTGAGGAGTGTGACTGTGTGTGCAGAGGAG 1178
|||||
117 rThrGlyGly 120
|||||
1179 CACAGGAGGA 1188
|||||
seq_name: gb_pat:AX118785

seq_documentation_block:
LOCUS AX118785 1760 bp DNA PAT 11-MAY-2001
DEFINITION Sequence 1 from Patent WO0128586.
ACCESSION AX118785
VERSION AX118785.1 GI:14035734
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1760)
AUTHORS Gilbertson,D.G.
TITLE Method of treating fibrosis
JOURNAL Patent: WO 0128586-A 1 26-APR-2001;
ZymoGenetics, Inc. (US)
FEATURES
source
1..1760
/organism="Homo sapiens"
/db_xref="taxon:9606"
154..1191
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC38478.1"
/db_xref="GI:14035735"
/translation="MSLFGLLLLTSALACQROGTQAEISNLSSKFQSSNKKEQNGVQDP
QHERITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQLTDFERFGLDEPDD
ICKYDFVEVEEPSDGTILGRWCGSTPGKQISKGNIIRIFVDFEYFPSEPFCIHY
NIVMPQTEAVSPVLPSPALPDLLNNAITAFSTLEDLIRYLEPERWQDLDELRYR
TWOLGKAFVFGKRSRVVDNLITFEVRLYSCTPRNFVSIREELKRTDTIIFWPGCLL
VKRCGNCACCLHNCNCCQVPSKVKYKHEVLQLRPKYGVRLHKLHSLTDVALEHHEE
CDCVCRGSGTGG"
BASE COUNT 494 a 373 c 411 g 482 t
ORIGIN

alignment_scores:
Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_226_345 x AX118785
Align seg 1/1 to: AX118785 from: 1 to: 1760
1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
829 GCCTTTGTTTTTGGAGAAAATCCAGAGTGGTGGATCTGAACCTTCAAC 878
|||||
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||
879 AGAGGAGGTGAAGATTATACAGCTGCACACCTCGTAACCTTCAGTGTCCA 928
|||||
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||
929 TAAGGGAAGAACTAAAGAGAACCATACCATTTCTGCCAGGTGTCTC 978
|||||
51 LeuValLysArgCysGlyLysAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
979 CTGGTTAAACGCTGTGTGGGAACTGTGCCTGTGTCTCCACAATTCGCA 1028
|||||
67 nGluCysGlnCysValProSerLysValThrLysLysThrHisGluValL 84
|||||

```

```

1029 TGAATGTCATGTGTCTCCCAAGCAAAAGTTACTAAAAAATACCAGAGGTCC 1078
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
1079 TTCAGTTGAGACCAAGACCGGTGTGTGAGGGATTGCACAATCACTCACC 1128
|||||
101 AspValAlaLeuGluHisGluCysAspCysValCysArgGlySe 117
|||||
1129 GACGTGGCCCTGGAGCACCATTGAGGAGTGTGACTGTGTGTGCAGAGGAG 1178
|||||
117 rThrGlyGly 120
|||||
1179 CACAGGAGGA 1188
|||||
seq_name: gb_pr:AF260738

seq_documentation_block:
LOCUS AF260738 1804 bp mRNA PRI 17-JUL-2001
DEFINITION Homo sapiens platelet-derived growth factor c (PDGFC) mRNA,
complete cds.
ACCESSION AF260738
VERSION AF260738.1 GI:14009503
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1804)
AUTHORS Gilbertson,D.G., Duff,M.E., West,J.W., Kelly,J.D., Sheppard,P.O.,
Hofstrand,P.D., Gao,Z., Shoemaker,K., Bukowski,T.R., Moore,M.,
Feldhaus,A.L., Humes,J.M., Palmer,T.E. and Hart,C.E.
TITLE Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor
That Binds to PDGF alpha and beta Receptor
JOURNAL J. Biol. Chem. 276 (29), 27406-27414 (2001)
MEDLINE 21347863
PUBMED 11297552
REFERENCE
2 (bases 1 to 1804)
AUTHORS Gao,Z., Hart,C., Piddington,C., Sheppard,P., Shoemaker,K.,
Gilbertson,D., West,J. and O'Hara,P.J.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2000) Biomolecular Informatics, ZymoGenetics,
Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA
FEATURES
Location/Qualifiers
1..1804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4q28.3"
1..1804
/gene="PDGFC"
163..1200
/gene="PDGFC"
/note="PDGF-C; ZVEGF3"
/codon_start=1
/product="platelet-derived growth factor C"
/protein_id="AAK51637.1"
/db_xref="GI:14009504"
/translation="MSLFGLLLLTSALAGORQGTQAEISNLSSKFQSSNKKEQNGVQDP
QHERITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQLTDFERFGLDEPDD
ICKYDFVEVEEPSDGTILGRWCGSTPGKQISKGNIIRIFVDFEYFPSEPFCIHY
NIVMPQTEAVSPVLPSPALPDLLNNAITAFSTLEDLIRYLEPERWQDLDELRYR
TWOLGKAFVFGKRSRVVDNLITFEVRLYSCTPRNFVSIREELKRTDTIIFWPGCLL
VKRCGNCACCLHNCNCCQVPSKVKYKHEVLQLRPKYGVRLHKLHSLTDVALEHHEE
CDCVCRGSGTGG"
BASE COUNT 531 a 375 c 416 g 482 t
ORIGIN

alignment_scores:
Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

```

alignment_block:

US-09-457-066-2_COPY_226_345 x AF260738

Align seg 1/1 to: AF260738 from: 1 to: 1804

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
 838 GCTTTTGTGTTTGGAGAAAATCCAGAGTGTGGATCTGAACCTCTTAAC 887
 17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
 888 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCAGTGTCCA 937
 34 leArgGluGluLeuLysArgThrAspThrIlePheTyrProGlyCysLeu 50
 938 TAAGGAGAGAACTAAAGAGAACCATACCATTTTCTGCCAGGTGTCTC 987
 51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
 988 CTGGTTAAACCGTGTGTGGGAACGTGCTGCTGTCTCCACAATTGCCAA 1037
 67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
 1038 TGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCACGAGGTCC 1087
 84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
 1088 TTCAGTTGAGACCAAGACCGGTGTACGGGAGTTGCACAAATCACTACC 1137
 101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlyse 117
 1138 GACGTGCCCTCGAGCACCATGAGGAGTGTGACTGTGTGTCCAGAGGGAG 1187
 117 rThrGlyGly 120
 1188 CACAGGAGGA 1197

seq_name: gb_pr:AB033831

seq_documentation_block:

LOCUS AB033831 1817 bp mRNA PRI 26-JUL-2000
 DEFINITION Homo sapiens hSCDGF mRNA for spinal cord-derived growth factor, complete cds.
 ACCESSION AB033831
 VERSION AB033831.1 GI:9392293
 KEYWORDS spinal cord-derived growth factor; scdGF gene.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (sites)
 Hamada,T., Ui-Tei,K. and Miyata,Y.
 A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family(1)
 FEBS Lett. 475 (2), 97-102 (2000)
 JOURNAL MEDLINE 20317014
 REFERENCE 2 (bases 1 to 1817)
 Hamada,T., Ui-Tei,K. and Miyata,Y.
 Direct Submission
 TITLE Submitted (25-OCT-1999) to the DDBJ/EMBL/GenBank databases.
 JOURNAL Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan
 (E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)

FEATURES

source

1. 1817
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /dev_stage="embryo"
 /tissue_type="brain"
 327..1364
 /gene="hSCDGF"
 327..1364

gene

CDS

/gene="hSCDGF"
 /codon_start=1
 /product="spinal cord-derived growth factor"
 /protein_id="BAB03266.1"
 /db_xref="GI:9392294"

/translation="MSLFLGLLLLSALAGORQGTQASNLSSKTFQSSNKEQNGVQDP
 QHERITVSTNGSIHSRPFPHYPRNTVLVWRLVAEENWVQILTFDERFLEDEDD
 ICKYDFVEVEEPSDGTILGRWCGSGTVPGKOISKGNQIRIRFVDEVPFSPGFCIH
 NIVMPOFTEAVSPVSPALPLDLNNAITAFSTLEDLIRYLEPERWQLOLEDLYRP
 TWQLLGRKAFVGRKSRVVDNLNLTVEEVRLYSCTPRNFSYSIREELKRTDTTFWPGCLL
 VKRCGNCACCLHNCNECCQVPSKTRKYHQLQIRPKTVGRGLHKLSDVALEHHEE
 CDCVCRGSGTG"

BASE COUNT 501 a 412 c 424 g 477 t 3 others
 ORIGIN

alignment_scores:

Quality: 666.00 Length: 120
 Ratio: 5.550 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_226_345 x AB033831

Align seg 1/1 to: AB033831 from: 1 to: 1817

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
 1002 GCTTTTGTGTTTGGAGAAAATCCAGAGTGTGGATCTGAACCTCTTAAC 1051
 17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
 1052 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCAGTGTCCA 1101
 34 leArgGluGluLeuLysArgThrAspThrIlePheTyrProGlyCysLeu 50
 1102 TAAGGAGAGAACTAAAGAGAACCATGACTTTTCTGGCAGGTGTCTC 1151
 51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
 1152 CTGGTTAAACCGTGTGTGGGAACCTGTGCTGTGTCTCCACAATTGCCAA 1201
 67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
 1202 TGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCACGAGGTCC 1251
 84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
 1252 TTCAGTTGAGACCAAGACCGGTGTCCAGGGATTGCACAAATCACTCAC 1301
 101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlyse 117
 1302 GACGTGCCCTCGAGCACCATGAGGAGTGTGACTGTGTGTCCAGAGGGAG 1351
 117 rThrGlyGly 120
 1352 CACAGGAGGA 1361

seq_name: gb_pr:AF244813

seq_documentation_block:

LOCUS AF244813 2152 bp mRNA PRI 01-JUL-2000
 DEFINITION Homo sapiens platelet-derived growth factor C mRNA, complete cds.
 ACCESSION AF244813
 VERSION AF244813.1 GI:8886883
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2152)
 Li,X., Ponten,A., Aase,K., Karlsson,L., Abramson,A., Untela,M., Backstrom,G., Hellstrom,M., Bostrom,H., Li,H., Soriano,P.,

Betsholtz,C., Heidlin,C.-H., Alitalo,K., Ostman,A. and Eriksson,U.
 PDGF-C is a novel protease-activated ligand for the PDGF alpha
 receptor
 Nat. Cell Biol. (2000) In press
 2 (bases 1 to 2152)
 Eriksson,U., Aase,K., Li,X. and Ponten,A.
 Direct Submission
 Submitted (14-MAR-2000) Ludwig Institute for Cancer Research,
 Nobels vag 3 P.O.Box 240, Stockholm S-171 77, Sweden
 FEATURES
 Location/Qualifiers
 1..2152
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /tissue_type="lung"
 /dev_stage="fetal"
 189..1226
 /function="ligand and agonist for platelet-derived growth
 factor receptor alpha (PDGFRAalpha)"
 /note="PDGF-C; member of the PDGF/VEGF growth factor
 family; contains N-terminal CUB domain and the C-terminal
 PDGF/VEGF-like domain"
 /codon_start=1
 /product="platelet-derived growth factor C"
 /protein_id="AAF80597.1"
 /db_xref="GI:8886884"
 621 a 424 c 476 g 630 t 1 others
 BASE COUNT
 ORIGIN
 alignment_scores:
 Quality: 666.00 Length: 120
 Ratio: 5.550 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-457-066-2_COPY_226_345 x AF244813 ..
 Align seg 1/1 to: AF244813 from: 1 to: 2152

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
 |||||
 864 GCCTTTGTTTTGGAGAAAAATCCAGAGTGGTGATCTGAACCTTCTAAC 913
 17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
 |||||
 914 AGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGCCA 963
 34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
 |||||
 964 TAAGGAAGAACTAAAGAACCACTGACCATTTTCTGCCAGGTGTCTC 1013
 51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
 |||||
 1014 CTGGTTAAACGCTGTGGTGGAACTGTGCCTGTGTCTCCACAATTGCAA 1063
 67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
 |||||
 1064 TGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCACGAGTCC 1113
 84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
 |||||
 1114 TTCAGTTGACCAAGAACCGGTGTACGGGGATTGCACAAATCACTCAC 1163
 101 AspValAlaLeuGluHisHisGluCysAspCysValCysArgGlySe 117
 |||||
 1164 GACGTGGCCCTGGAGCAACCATGAGGAGTGTGACTGTGTGTGCAGAGGAG 1213

117 rThrGlyGly 120
 |||||
 1214 CACAGGAGGA 1223

seq_name: gb_pat:AX047650

seq_documentation_block:
 LOCUS AX047650 2849 bp DNA PAT 15-DEC-2000
 DEFINITION Sequence 9 from Patent WO0070050.
 ACCESSION AX047650
 VERSION AX047650.1 GI:11876693
 KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2849)
 AUTHORS Baker,K.P., Chen,J., Ferrara,N., Fong,S., Goddard,A., Gurney,A.L.,
 Hillan,K.J., Kuo,S.S., Tumas,D. and Wood,W.I.
 TITLE Compositions and methods for the treatment of immune related
 diseases

JOURNAL Patent: WO 0070050-A 9 23-NOV-2000;

Genentech, Inc. (US)

FEATURES Location/Qualifiers

source 1..2849

/organism="Homo sapiens"

/db_xref="taxon:9606"

2715

/note="unknown base"

BASE COUNT 851 a 528 c 619 g 850 t 1 others

ORIGIN

alignment_scores:

Quality: 666.00 Length: 120

Ratio: 5.550 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_226_345 x AX047650 ..

Align seg 1/1 to: AX047650 from: 1 to: 2849

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
 |||||
 960 GCCTTTGTTTTGGAGAAAAATCCAGAGTGGTGATCTGAACCTTCTAAC 1009
 17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
 |||||
 1010 AGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGCCA 1059
 34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
 |||||
 1060 TAAGGAAGAACTAAAGAACCACTGACCATTTTCTGCCAGGTGTCTC 1109
 51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
 |||||
 1110 CTGGTTAAACGCTGTGGTGGAACTGTGCCTGTGTCTCCACAATTGCAA 1159
 67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
 |||||
 1160 TGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCACGAGTCC 1209
 84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
 |||||
 1210 TTCAGTTGACCAAGAACCGGTGTACGGGGATTGCACAAATCACTCAC 1259
 101 AspValAlaLeuGluHisHisGluCysAspCysValCysArgGlySe 117
 |||||
 1260 GACGTGGCCCTGGAGCAACCATGAGGAGTGTGACTGTGTGTGCAGAGGAG 1309
 117 rThrGlyGly 120

```

|||||
1310 CACAGGAGGA 1319
seq_name: gb_pr:AF091434
seq_documentation_block:
LOCUS AF091434 3007 bp mRNA PRI 22-JUN-2000
DEFINITION Homo sapiens secretory growth factor-like protein fallotein mRNA,
complete cds.
ACCESSION AF091434
VERSION AF091434.1 GI:6002592
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3007)
AUTHORS Tsai,Y.-J., Lee,R.K.-K., Lin,S. and Chen,Y.
TITLE Identification of a novel platelet-derived growth factor-like gene,
fallotein, in the human reproductive tract
JOURNAL Biochim. Biophys. Acta 1492 (1), 196-202 (2000)
MEDLINE 20461776
REFERENCE 2 (bases 1 to 3007)
AUTHORS Tsai,Y.-J., Lee,R.K.-K. and Lin,S.P.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1998) Dept. Medical Research, Mackay Memorial
Hospital, 45 Min Sheng Road, Tamshui, Taipei County 25115, Taiwan
FEATURES
source
1..3007
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="uterus"
492..1529
/codon_start=1
/evidence=not_experimental
/product="secretory growth factor-like protein fallotein"
/protein_id="AAF00049.1"
/db_xref="GI:6002593"
/translation="MSLFLGLLLTSLAGORGTQAESNLSSKFQSSNKQNGVQDP
QHERIITVSTGSIHSPFPHYPRNVLVRLVAVENWVQLTDFRGLDEPDD
ICKYDFVEEPEPSDTILRWCGSGTVPKGQISKGNIIRFVSDYFPPSEPGFCIH
NIVMPQTFEAVSPSLPPLDNLNNAITAFSTLEDLIRYLEPERWQDLDELRYR
TWLLGKAFAVFGKRSRVVDNLLEEVRLYSCTPRNFVSIRREELKRTDTIFWPGCLL
VKRCGNCACCLHNCNECQVPSKVTYKTYHEVLQRLPKTGVGRGLHSLTDVALEHHEE
CDCVCRGSTG"
polyA_signal 2974..2979
BASE COUNT 858 a 613 c 635 g 901 t
ORIGIN

alignment_scores:
Quality: 666.00 Length: 120
Ratio: 5.350 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_226_345 x AF091434
Align seg 1/1 to: AF091434 from: 1 to: 3007
1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
1167 GCCTTTGTTTTGGAGAAATCCAGAGTGGTGATCTGACCTCTAAC 1216
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||
1217 AGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGCCA 1266
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||
1267 TAAGGAAGAACTAAAGAACCGATACCATTTCTGCCAGGTTGCTC 1316
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisasnCysAs 67
|||||
1317 CTGGTTAAACGCTGTGGTGGAACTGTGCTGTCTGCACAAATGCCAA 1366
67 nGluCysGlnCysValProSerLysValThrLysLysLysTyrHisGluValL 84
|||||
1367 TGAATGTCAATGTGCCCCAAGCAAGATTACTAAAAAATACCAGAGGTCC 1416
84 euGluLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
1417 TTCAGTTGAGACCAAGACCGGTGTCCAGGGGATTGCACAAATCCTCACC 1466
101 AspValAlaLeuGluHisGluGluCysAspCysValCysArgGlySe 117
|||||
1467 GACGTGGCCCTCGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAG 1516
117 rThrGlyGly 120
|||||
1517 CACAGGAGGA 1526
seq_name: gb_ro:AF117608
seq_documentation_block:
LOCUS AF117608 2692 bp mRNA ROD 02-JAN-2000
DEFINITION Mus musculus fallotein mRNA, complete cds.
ACCESSION AF117608
VERSION AF117608.1 GI:6652867
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 2692)
AUTHORS Tsai,Y.-J., Lee,R.K.-K., Chen,Y.-H., Lin,S.-P. and Cheng,W.T.-K.
TITLE cDNA cloning of fallotein from mouse ovary
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2692)
AUTHORS Tsai,Y.-J., Lee,R.K.-K., Chen,Y.-H., Lin,S.-P. and Cheng,W.T.-K.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-1999) Medical Research, Mackay Memorial Hospital,
45 Min Sheng Road, Tamshui, Taipei 25115, Taiwan
FEATURES
source
1..2692
/organism="Mus musculus"
/db_xref="taxon:10090"
/sex="female"
/tissue_type="ovary"
/db_stage="adult"
198..1235
/notes="putative secretory protein"
/codon_start=1
/evidence=not_experimental
/product="fallotein"
/protein_id="AAF22516.1"
/db_xref="GI:6652868"
/translation="MLLGLLLTSLAGORTGTRAESNLSSKLQSLSSDKQNGVQDP
RHERVYIISNGSIHSPKFPHTYPRNVLVRLVAVDENVRIQLTDFRGLDEPDD
ICKYDFVEEPEESDGSVLGWCGSGTVPKGQISKGNIIRFVSDYFPPSEPGFCIH
YTIIMQVTFETSPSLPPLDNLNNAITAFSTLEDLIRYLEPERWQDLDELRYR
TWLLGKAFLYKKSKVYNLNLKKEVKLYSCTPRNFVSIRREELKRTDTIFWPGCLL
VKRCGNCACCLHNCNECQVPRVKTKYHEVLQRLPKTGVGRGLHSLTDVALEHHEE
CDCVCRGNAGG"
polyA_signal 2682..2687
BASE COUNT 754 a 576 c 617 g 745 t
ORIGIN

alignment_scores:
Quality: 624.00 Length: 120
Ratio: 5.288 Gaps: 0
Percent Similarity: 98.333 Percent Identity: 90.833

alignment_block:
US-09-457-066-2_COPY_226_345 x AF117608

```

Align seg 1/1 to: AF117608 from: 1 to: 2692

```
1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
873 GCYTTCTGTATGGGAAACAAAGAGTGTGATCTGAATCTCCTCAA 922

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
923 GGAAGAGGTAACCTACAGCTGCACACCCCGGAACCTCTCAGTGTCCA 972

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
973 TACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGCCAGGTGTCTC 1022

51 LeuValLysArgCysGlyGlyValAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1023 CTGCTCAAGCGCTGTGGAGGAATGTGCTGTCTCCATAATTCGCAA 1072

67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1073 TGAATGTCAGTGTCTCCACAGCTAAAGTTACAAAAAGTACCATGAGGTCC 1122

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1123 TTCAGTTGAGACCAACCAACTGGAGTCAAGGATTCGATAAGTCACTCACT 1172

101 AspValAlaLeuGluHisGluGluCysAspCysValCysArgGlySe 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1173 GATGTGCTCTGGAAACCAACGAGGAATGTGACTGTGTGTAGAGAAA 1222

117 rThrGlyGly 120
|||||:|||||
1223 CGCAGGAGGG 1232
```

seq_name: gb_ro:AF266467

```
seq_documentation_block:
LOCUS AF266467 3512 bp mRNA ROD 02-JUN-2001
DEFINITION Mus musculus platelet-derived growth factor C (pdgfc) mRNA,
complete cds.
ACCESSION AF266467
VERSION AF266467.1 GI:14279331
KEYWORDS .
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Gao,Z., Hart,C., Piddington,C., Sheppard,P., Shoemaker,K.,
Gilbertson,D., West,J. and O'Hara,P.J.
Platelet-derived growth factor C (PDGF-C), a novel growth factor
that binds to PDGF alpha receptor
Unpublished
JOURNAL 2 (bases 1 to 3512)
REFERENCE Gao,Z., Hart,C., Piddington,C., Sheppard,P., Shoemaker,K.,
AUTHORS Gilbertson,D., West,J. and O'Hara,P.J.
Direct Submission
TITLE Submitted (10-MAY-2000) Biomolecular Informatics, ZymoGenetics,
JOURNAL Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA
FEATURES
Location/Qualifiers
1..3512
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
1..3512
/gene="pdgfc"
1022..2059
/gene="pdgfc"
/note="PDGF-C/zvegf3"
/codon_start=1
/product="platelet-derived growth factor C"
/protein_id="AAK58566.1"
source
```

```
gene
CDS
```

```
/db_xref="GI:14279332"
/translation="MLLGLLLLTSLAAGQRTGTPAESNLSKQLSLSDKQNGVQDP
RHERVITISNGSIHSPKPHITYPRNMVLYWRLVAVDENRIQITFDERFLEDPEDD
ICKYDFVEEPEPSDGLRGWCGSGTVPKQSGNHIRIRFVSDVFPSPGFCIH
SITMPQVETETSPSVLPSSLSLDLANNATFATLELIRYLEPDRWQVLDLSLYK
TWQLLGNALYLGKSKVYNLNLKKEVKLYSCTPRNFSVSIREELKRTDTTFWGCCLL
VKRCGNCACCLHNCNEQCQVPRKTKYHEVLQLRPKTVGKGLHKLSLTDVLEHHEE
CDCVCRGNAGG"
BASE COUNT 850 a 920 c 861 g 881 t
ORIGIN
```

```
alignment_scores:
Quality: 624.00 Length: 120
Ratio: 5.288 Gaps: 0
Percent Similarity: 98.333 Percent Identity: 90.833
alignment_block:
US-09-457-066-2_COPY_226_345 x AF266467
Align seg 1/1 to: AF266467 from: 1 to: 3512
```

```
1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1697 GCTTTCTCTATGGGAAAAAAGCAAGTGGTGAATCTGAATCTCCTCAA 1746

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1747 GGAAGAGGTAAACTCTACAGCTGCACACCCCGGAACCTCTCAGTGTCCA 1796

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1797 TACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGCCAGGTGTCTC 1846

51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1847 CTGGTCAAGCGCTGTGCAGGAAATTTGCTGTGTCTCATAAATTCGCAA 1896

67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1897 TGAATGTCTAGTGTCTCCACAGTAAAGTTACAAAAAGTACCATGAGGTCC 1946

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1947 TTCAGTTGAGACCAACCAACTGGAGTCAAGGATTCATAGTCACTCACT 1996

101 AspValAlaLeuGluHisGluGluCysAspCysValCysArgGlySe 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1997 GATGTGGCTCTGGAACACCCAGGGAATGTGACTGTGTGTAGAGGAAA 2046

117 rThrGlyGly 120
|||||:|||||
2047 CGCAGGAGGG 2056
```

seq_name: gb_pat:AX044520

```
seq_documentation_block:
LOCUS AX044520 3571 bp DNA PAT 24-NOV-2000
DEFINITION Sequence 34 from Patent WO0066736.
ACCESSION AX044520
VERSION AX044520.1 GI:11343375
KEYWORDS .
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3571)
AUTHORS Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.
TITLE Growth factor homolog zvegf4
JOURNAL Patent: WO 0066736-A 34 09-NOV-2000;
ZymoGenetics, Inc. (US)
FEATURES
Location/Qualifiers
1..3571
```

```
REFERENCE 1 (bases 1 to 3571)
AUTHORS Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.
TITLE Growth factor homolog zvegf4
JOURNAL Patent: WO 0066736-A 34 09-NOV-2000;
ZymoGenetics, Inc. (US)
FEATURES
Location/Qualifiers
source 1..3571
```

[illegible]

```

VERSION      AB033830.1 GI:11994799
KEYWORDS     Spinal cord-derived growth factor; SCDGF.
SOURCE       Rattus norvegicus (strain:Wistar) Adult Kidney cDNA to mRNA.
ORGANISM     Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE    1 (sites)
AUTHORS     Hamada,T., Ui-Tei,K., Imaki,J. and Miyata,Y.
TITLE       Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
              SCDGF/PDGF-C/Fallotelin
JOURNAL     Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)
PUBMED      11162582
REFERENCE    2 (bases 1 to 1116)
AUTHORS     Hamada,T., Ui-Tei,K. and Miyata,Y.
TITLE       Direct Submission
JOURNAL     Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,
              Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo
              113-8602, Japan (E-mail:t-hamada@nms.ac.jp,
              Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)
FEATURES     Location/Qualifiers
              1..1116
                /organism="Rattus norvegicus"
                /strain="Wistar"
                /db_xref="taxon:10116"
                /tissue_type="Kidney"
                /dev_stage="Adult"
              1..1038
                /gene="rScdgf"
              1..1038
                /gene="rScdgf"
                /codon_start=1
                /product="spinal cord-derived growth factor"
                /protein_id="BAB1994800"
                /db_xref="GI:11994800"
                /translation="MLLGGLLLTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDP
              RHERVVTISNGSIHSPKFPHTYPRNVLVRLVAVDENVRVQLTFDERFGLDEPDD
              LCKYDFVEVEPSDGLVRCWCGSTVPGKSTVGNHIRIRFVSDVFPSPGFCIHY
              SILMPQVETTSVPLPSALSLLDLNNAVTAFSTVEELIRLEPDRWQIDLDLYKP
              TWPLLGKAFVLGKKSKANVNLKKEVKLYSCTPRNFSVIREELKRTDITFPWGCIL
              VRCGNCACCLHNCNCCQVPRKVTYKHYEVLQRLPKIGVGLHLSLTDVALEHHEE
              CDCVCRGNTEG"
BASE COUNT   301 a 267 c 286 g 262 t
ORIGIN
alignment_scores:
  Quality: 611.00      Length: 120
  Ratio: 5.267         Gaps: 0
  Percent Similarity: 96.667 Percent Identity: 89.167
alignment_block:
  US-09-457-066-2_COPY_226_345 x AB033830
  Align seg 1/1 to: AB033830 from: 1 to: 1116
1 AlaphevalPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
676 GCTTTCCTGCTGAGGAAAAAGCAACGCGTGAATCTGACACCTCTCAA 725
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
726 AGAAGAGGTAAACTTTACAGCTGCACACCCCGGAACCTTCTCTGTGTCCA 775
34 leArgGluGluLeuLysArgThrAspThrIlePheTyrProGlyCysLeu 50
776 TACGGGAAGAGCTAAAGAGCAGACACCATATCTGCGCAGGTGTCTC 825
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
826 CTGGTCAAGCGCTGTGGAGGAATGTGCTGTGCTCCATAATTCGAA 875
67 nGluCysGlnCysValProSerLysValThrLysLysThrHisGluValL 84

```

```

|||||
876 TGAATGTCAAGTGTGTCCTCCACGTAAGTTACAAAAAGTACCATTGAGGTCC 925
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
926 TTCAGTTGAGACCAAAAATTTGGAGTCAAGGATTGCATAGTCGCTCACC 975
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlyse 117
|||||
976 GATGTGGCCCTGGACACCATGAGGAATGTGACTGTGTGTGTAGAGGAAA 1025
117 rThrGlyGly 120
|||||
1026 CACAGAAGGG 1035
seq_name: gb_ro:AF286725
seq_documentation_block:
LOCUS      AF286725      1038 bp      mRNA      ROD      23-AUG-2000
DEFINITION Mus musculus platelet-derived growth factor c (Pdgfc) mRNA,
              complete cds.
ACCESSION  AF286725
VERSION    AF286725.1 GI:9652343
KEYWORDS   house mouse.
SOURCE     Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 1038)
AUTHORS    Ding,H., Wu,X., Kim,I., Tam,P.P., Koh,G.Y. and Nagy,A.
TITLE      The mouse pdgfc gene: dynamic expression in embryonic tissues
              during organogenesis
JOURNAL     Mech. Dev. 96 (2), 209-213 (2000)
MEDLINE    20417814
REFERENCE  2 (bases 1 to 1038)
AUTHORS    Ding,H., Wu,X., Tam,P.P.L. and Nagy,A.
TITLE      Direct Submission
JOURNAL     Submitted (12-JUL-2000) Samuel Lunenfeld Research Institute, Mount
              Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
              Canada
FEATURES     Location/Qualifiers
              1..1038
                /organism="Mus musculus"
                /strain="Swiss-Webster/NIH"
                /db_xref="taxon:10090"
              1..1038
                /gene="Pdgfc"
              1..1038
                /gene="Pdgfc"
                /note="PDGFC; similar to PDGF/VEGF"
                /codon_start=1
                /product="platelet-derived growth factor c"
                /protein_id="AAF91483.1"
                /db_xref="GI:9652344"
                /translation="MLLGLLLTSALAGQRTGTRAESNLSSKQLSSDKQNGVQDP
              RHERVVTISNGSIHSPKFPHTYPRNVLVRLVAVDENVRVQLTFDERFGLDEPDD
              ICKYDFVEVEPSDGLVRCWCGSTVPGKSTVGNHIRIRFVSDVFPSPGFCIHY
              SIIMPOVETTSVPLPSALSLLDLNNAVTAFSTVEELIRLEPDRWQIDLDLYKP
              TWOLGKAFVLVKKSVNLLKKEVKLYSCTPRNFSVIREELKRTDITFPWGCIL
              VKRCGNCACCLHNCNCCQVPRKVTYKHYEVLQRLPKIGVGLHLSLTDVALEHHEE
              CDCVCRGNAGG"
BASE COUNT   287 a 230 c 274 g 247 t
ORIGIN
alignment_scores:
  Quality: 608.00      Length: 120
  Ratio: 5.241         Gaps: 0
  Percent Similarity: 96.667 Percent Identity: 89.167
alignment_block:
  US-09-457-066-2_COPY_226_345 x AF286725

```


OM of: US-09-457-066-2_COPY_226_345 to: N_Geneseq_1101:* out_format : pfs

Date: Jan 15, 2002 11:08 PM

About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

```

MODEL=frnane_p2n_model DEV=x1h
-Q/cgml21/USPTO_spool/usfap457066/runat_15012002_132155_1424
-DB=N_Genesec_1101 -QFMT=fastap -SUFFIX=mg -GAPOF=12.000
-GAPEX=4.500 -MINMATCH=0.100 -LOAPCL=0.000 -LOOPEXT=0.000
-GAPOF=4.500 -QGAPEX=0.050 -XGAPOF=10.000 -XGAPEX=0.500
-FCAPOF=6.000 -FGAPEX=7.000 -XGAPOF=10.000 -YGAPEX=0.500
-DELOP=6.000 -DELEX=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DICALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-DEV=US09457066.ecgml_1_258 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLXPY -WAIT_THREADS=1

```

Search information block:

SEARCH INFORMATION BLOCK.
Query: US-09-457-066-2 COPY 226 345

Query length: 120

Database: N_Geneseq_1101:*

Database sequences: 930621

Database length: 428662619

```
Search time (sec): 100.840000
```

score list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SIDS2/cgdata/geneseq/NA2000.DAT:AAA15140	+	666.00	1341.19	666.00	1.3e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA1985	+	666.00	1341.18	666.00	1.3e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA1983	+	666.00	1340.82	666.00	1.3e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA1984	+	666.00	1340.82	666.00	1.3e-66
SIDS2/cgdata/geneseq/NA2001.DAT:AAF82259	+	666.00	1339.15	666.00	1.6e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA19155	+	666.00	1338.07	666.00	1.9e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAAC81582	+	666.00	1336.20	666.00	2.4e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA51498	+	666.00	1336.20	666.00	2.4e-66
SIDS2/cgdata/geneseq/NA2001.DAT:AAAD04649	+	666.00	1336.20	666.00	1.76e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA12523	+	666.00	1334.31	666.00	3.0e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA19151	+	666.00	1332.62	666.00	2.475e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA19190	+	666.00	1331.83	666.00	2.668e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA19152	+	666.00	1331.42	666.00	2.776e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA52458	+	666.00	1331.41	666.00	2.779e-66
SIDS2/cgdata/geneseq/NA1999.DAT:AAZ23691	+	666.00	1331.23	666.00	3.45e-66
SIDS2/cgdata/geneseq/NA2001.DAT:AAAD06812	+	666.00	1331.23	666.00	2.827e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAAA7452	+	666.00	1331.18	666.00	4.5e-66
SIDS2/cgdata/geneseq/NA1999.DAT:AAZ34296	+	666.00	1331.14	666.00	2.849e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AACT8582	+	666.00	1331.14	666.00	2.849e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAA885179	+	666.00	1331.14	666.00	2.849e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAAC59579	+	666.00	1331.14	666.00	2.849e-66
SIDS2/cgdata/geneseq/NA2001.DAT:AAAAT7621	+	666.00	1331.14	666.00	4.5e-66
SIDS2/cgdata/geneseq/NA2001.DAT:AAAS21386	+	666.00	1331.14	666.00	2.849e-66
SIDS2/cgdata/geneseq/NA2001.DAT:AAAC90564	+	666.00	1331.14	666.00	2.849e-66
SIDS2/cgdata/geneseq/NA2001.DAT:AAAC89662	+	666.00	1331.14	666.00	2.849e-66
SIDS2/cgdata/geneseq/NA2001.DAT:AACT97404	+	666.00	1331.14	666.00	4.5e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAZ48599	+	666.00	1331.11	666.00	4.6e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAAC54426	+	666.00	1330.97	666.00	4.6e-66
SIDS2/cgdata/geneseq/NA1999.DAT:AAAB6352	+	666.00	1330.97	666.00	4.6e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAAF18314	+	666.00	1330.30	666.00	5.1e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAAL12524	+	660.00	1325.35	660.00	9.5e-66
SIDS2/cgdata/geneseq/NA2000.DAT:AAAZ48600	+	650.00	1298.61	650.00	2.9e-64
SIDS2/cgdata/geneseq/NA2000.DAT:AAA1986	+	646.00	1308.49	646.00	8.3e-65
SIDS2/cgdata/geneseq/NA2000.DAT:AAAL12525	+	624.00	1252.12	624.00	1.1e-61
SIDS2/cgdata/geneseq/NA2000.DAT:AAAC81583	+	624.00	1242.83	624.00	3.8e-61
SIDS2/cgdata/geneseq/NA2000.DAT:AAA51527	+	624.00	1242.83	624.00	3.8e-61
SIDS2/cgdata/geneseq/NA2001.DAT:AAAD04650	+	624.00	1242.83	624.00	3.8e-61
SIDS2/cgdata/geneseq/NA2000.DAT:AAA1981	+	607.00	1223.47	607.00	4.5e-60
SIDS2/cgdata/geneseq/NA2000.DAT:AAA1982	+	607.00	1215.74	607.00	1.2e-59
SIDS2/cgdata/geneseq/NA2000.DAT:AAA19136	+	607.00	1214.77	607.00	1.4e-59

CC be used to modulate neurite growth and development of the nervous system,
CC and for treating neurodegenerative diseases.

XX
SQ Sequence 1095 BP; 320 A; 227 C; 267 G; 281 T; 0 other;

alignment_scores:
Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_226_345 x AAA51540

Align seg 1/1 to: AAA51540 from: 1 to: 1095

1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
715 GCCTTTCTTTTGGAGAAATCCAGAGTGGTGATCTGAACCTTCTAAC 764

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||
765 AGAGGAGGTAGATTATACAGCTGCACACCTCGTAACCTTCAGTGTCCA 814

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||
815 TAAGGGAAGAACTAAACAGAACCATACCATTTCTGCCAGGTGTCTC 864

51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
865 CTGGTTAAACGCTGTGTGGGAATGTCCTCTGTCTCCACAATTGCAA 914

67 nGluGlnCysValProSerLysValThrLysLysThrHisGluValL 84
|||||
915 TGAATGTCATGTCTCCCAAGCAAGTTACTAAAAATACACAGGTCC 964

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
965 TTCAGTTGACCAAGACCGGTGTACGGGATGTCACAAATCACTACC 1014

101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlyse 117
|||||
1015 GACGTGCCCTGGAGCACCATGAGGAGTGTCACTGTGTGTGCAGGGAG 1064

117 rThrGlyGly 120
|||||
1065 CACAGGAGGA 1074

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT:AAA71985

seq_documentation_block:

ID AAA71985 standard; DNA; 1096 BP.

XX

AC AAA71985;

XX

DT 19-JAN-2001 (first entry)

XX

DE Human VEGF-X DNA for expression in E. coli systems.

XX

KW VEGF-X; vascular endothelial growth factor; human; vulnery;

KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

OS Homo sapiens.

XX

Key Location/Qualifiers

FT CDS 3..1070

FT /*tag= a

FT /product= "VEGF-X"

XX

PN WO200037641-A2.

XX

PD 29-JUN-2000.

XX

PF 21-DEC-1999; 99WO-US30503.

XX

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX

PA (JANC) JANSSEN PHARM NV.

XX

PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX

DR WPI; 2000-442669/38.

DR P-PSDB; AAB10641.

XX

PT New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX

PS Disclosure; Fig 21; 127pp; English.

XX

CC This invention describes a novel vascular endothelial growth factor-X

CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has

CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and

CC antidiabetic activity and acts as an angiogenesis and vascularization

CC regulator. An antisense molecule of the invention is useful for treating

CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

CC retinopathy by inhibiting angiogenic activity or inappropriate

CC vascularization including formation and proliferation of new blood

CC vessels, growth and development of tissues, tissue regeneration and organ

CC and tissue repair in a subject. The products of the invention are useful

CC for preparing medicaments for treating wounds such as dermal ulcers,

CC pressure sores, venous sores, diabetic ulcers and burns and to promote

CC skin graft growth, tissue repair, proliferation of new blood vessels,

CC tissue regeneration and organ repair by promoting angiogenic activity or

CC vascularization. This sequence encodes a human VEGF-X protein which can

CC be expressed in E. coli systems and which is described in the method of

CC the invention.

XX

SQ Sequence 1096 BP; 337 A; 225 C; 253 G; 281 T; 0 other;

alignment_scores:

Quality: 666.00 Length: 120

Ratio: 5.550 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_226_345 x AAA71985

Align seg 1/1 to: AAA71985 from: 1 to: 1096

1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
690 GCCTTTCTTTTGGAGAAATCCAGAGTGGTGATCTGAACCTTCTAAC 739

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||
740 AGAGGAGGTAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCA 789

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||
790 TAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGCCAGGTGTCTC 839

51 LeuValLysArgCysGlyCysAlaCysCysLeuHisAsnCysAs 67
|||||
840 CTGGTTAAACGCTGTGTGGGAACCTGTGCTGTCTCCACAATTGCAA 889

67 nGluCysGlnCysValProSerLysValThrLysLysThrHisGluValL 84
|||||

890 TGAATGTCATGTGTCCTCCAGCAAGTTACTATAAAATACACAGGTCC 939
 84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
 |||||
 940 TTCAGTTGAGACCAAGACCGGTCTCAGGGGATTGCACAAATCACTCACC 989
 101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
 |||||
 990 GACGTGGCCCTGGAGCACCATTGAGGAGTGTGACTGTGTGTGCAGAGGGAG 1039
 117 rThrGlyGly 120
 |||||
 1040 CACAGGAGGA 1049

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT:AAA71983

seq_documentation_block:

ID AAA71983 standard; DNA; 1134 BP.

XX AC

XX AC

XX AAA71983;

XX 19-JAN-2001 (first entry)

XX Human VEGF-X DNA for expression in mammalian systems.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

XX Homo sapiens.

PH Key Location/Qualifiers

FT CDS 10..1134

FT /*tag= a

FT /*product= "VEGF-X"

PN W0200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

XX 18-MAR-1999; 99US-0124967.

XX 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD., Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;

XX Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX P-PSDB; AAB10639.

XX New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure; Fig 19; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
 CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation and proliferation of new blood
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful

CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence encodes a human VEGF-X protein which can
 CC be expressed in mammalian systems and which is described in the method of
 CC the invention.

XX
 SQ Sequence 1134 BP; 324 A; 247 C; 269 G; 294 T; 0 other;

alignment_scores:
 Quality: 666.00 Length: 120
 Ratio: 5.550 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_226_345 x AAA71983

Align seg 1/1 to: AAA71983 from: 1 to: 1134

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
 |||||
 685 GCTTTTGTGTTTGGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAAC 734

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
 |||||
 735 AGAGGAGGTAGATTATACAGCTGCACACCTCTCACTTCTCAGTGTCCA 784

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
 |||||
 785 TAAAGGAAGAACTAAAGAGAACCGATACATTTTCTGGCCAGGTTGCTC 834

51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
 |||||
 835 CTGTTTAAACGCTGTGGTGGAACTGTGCCTTGTCTCCACAATTCGAA 884

67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluVal 84
 |||||
 885 TGAATGTCATGTTGCCCAAGCAAGTACTAAAAAATACACAGAGGTCC 934

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
 |||||
 935 TTCAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCACTCACC 984

101 AspValAlaLeuGluHisGluGluCysAspCysValCysArgGlySe 117
 |||||
 985 GACGTGGCCCTGGAGCACCATTGAGGAGTGTGACTGTGTGTGCAGAGGGAG 1034

117 rThrGlyGly 120

|||||

1035 CACAGGAGGA 1044

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT:AAA71984

seq_documentation_block:

ID AAA71984 standard; DNA; 1134 BP.

XX AC

XX AAA71984;

XX 19-JAN-2001 (first entry)

XX Human VEGF-X DNA for expression in Baculovirus/insect cell systems.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth; ds.
 XX Homo sapiens.

```

FH Key Location/Qualifiers
FT CDS 63..1127
FT /*tag= a
FT /product= "VEGF-X"
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC ) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI; 2000-442669/38.
DR P-PSDB; AAB10640.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Disclosure; Fig 20; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence encodes a human VEGF-X protein which can
CC be expressed in Baculovirus/insect cell systems and which is described in
CC the method of the invention.
XX
SQ Sequence 1134 BP; 339 A; 225 C; 254 G; 316 T; 0 other;

alignment_scores:
    Quality: 666.00 Length: 120
    Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_226_345 x AAA71984
Align seg 1/1 to: AAA71984 from: 1 to: 1134
1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
765 GCTTTTGTGAGAGAAATCCAGAGTGGTGGATCTGAACCTCTAAC 814
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
815 AGAGGAGGTAAGATTATACAGTCACACCTCGTAACCTCTCAGTGTCCA 864
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
865 TAAGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTGTCTC 914
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67

```

```

|||||
915 CTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTCTCCACAATTGCCAA 964
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValI 84
|||||
965 TGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAGAGGTCC 1014
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
1015 TTCAGTTGAGACCAAGACCGGTGTTCAGGGATTGCACAAATCACTCACC 1064
101 AspValAlaLeuGluHisGluGluCysAspCysValCysArgGlySe 117
|||||
1065 GACGTGGCCCTGGACCAACCATGAGGAGTGTGCTGTGTGCAGAGGGAG 1114
117 rThrGlyGly 120
|||||
1115 CACAGGAGGA 1124

seq_name: /SID52/gcgdata/geneseq/geneseq/NA2001.DAT:AAF82259
seq_documentation_block:
ID_ AAF82259 standard; DNA; 1328 BP.
XX
AC AAF82259;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human VEGF/PDGF-like factor nucleotide sequence.
XX
KW Human; VEGF/PDGF-like factor; vascular endothelial growth factor; VEGF;
KW platelet derived growth factor; PDGF; neovascularisation; disease; ds.
XX
OS Homo sapiens.
XX
PN JP2001017188-A.
XX
PD 23-JAN-2001.
XX
PF 24-APR-2000; 2000JP-0122994.
XX
PR 22-APR-1999; 99JP-0115516.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
PA (HERI-) HERIKKUSU KENKYUSHO KK.
XX
DR WPI; 2001-285410/30.
DR P-PSDB; AAB74028.
XX
PT New VEGF/PDGF-like factor useful for the development of treating agents
PT for diseases accompanied by accentuation of abnormal neovascularization
XX
PS Example 2; Page 37-39; 52pp; Japanese.
XX
CC The present sequence is a novel vascular endothelial growth factor
CC (VEGF)/platelet derived growth factor (PDGF)-like factor. The
CC invention relates to the present 345 amino acid sequence or
CC a sequence in which at least one amino acid is deleted, replaced or
CC added compared to the present sequence. The nucleotide sequence
CC encoding this protein may be integrated into a vector and used to
CC transform a host cell. The VEGF/PDGF-like factor may be used in the
CC development of agents for treating diseases associated with
CC abnormal neovascularisation.
XX
SQ Sequence 1328 BP; 372 A; 288 C; 324 G; 344 T; 0 other;

alignment_scores:
    Quality: 666.00 Length: 120
    Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

```

alignment_block:

US-09-457-066-2_COPY_226_345 x AAF82259

Align seg 1/1 to: AAF82259 from: 1 to: 1328

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
769 GCTTTTGTGTTTGGAGAAAAATCCAGAGTGGTGATCTGAACCTTCTAAC 818
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
189 AGAGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGCCA 868
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
869 TAAGGGAAGAACTAAGACACCGATACCATTTTCTGCCAGGTGTCTC 918
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
919 CTGGTTAAACGCTGTGGTGGAACTGTGCCTGTGTCTCCACAATTGCAA 968
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
969 TGAATGTCAATGTGCTCCCAAGCAAAAGTTACTAAAAAATACACGAGTCC 1018
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
1019 TTCAGTTGAGACCAAGACCGGTCTCAGGGGATTGCACAAATCACTACC 1068
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
1069 GACGTGGCCCTGGAGCACCATGAGGAGTGAGTGTGTGTGCAGAGGGAG 1118
117 rThrGlyGly 120
1119 CACAGGAGGA 1128

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AA71955

seq_documentation_block:

ID AA71955 standard; DNA; 1473 BP.

XX AA71955;

AC XX

DT 19-JAN-2001 (first entry)

XX Human VEGF-X DNA isolated from clones 4 and 7.

DE VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

XX Homo sapiens.

OS WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosielska A;

PI Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

DR P-PSDB; AAB10635, AAB10636.

XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Claim 4; Fig 9; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence encodes the human VEGF-X protein isolated
CC from clones 4 and 7 described in the method of the invention.

XX Sequence 1473 BP; 406 A; 321 C; 361 G; 385 T; 0 other;

alignment_scores:

Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_226_345 x AAA71955

Align seg 1/1 to: AAA71955 from: 1 to: 1473

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
932 GCTTTTGTGTTTGGAGAAAAATCCAGAGTGGTGATCTGAACCTTCTAAC 981
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
982 AGAGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGCCA 1031
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
1032 TAAGGGAAGAACTAAGACACCGATACCATTTTCTGCCAGGTGTCTC 1081
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
1082 CTGGTTAAACGCTGTGGTGGAACTGTGCCTGTGTCTCCACAATTGCAA 1131
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
1132 TGAATGTCAATGTGCTCCCAAGAAAGTTACTAAAAAATACACGAGGTCC 1181
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
1182 TTCAGTTGAGACCAAGACCGGTGTCCAGGGGATTGCACAAATCACTACC 1231
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
1232 GACGTGGCCCTGGAGCACCATGAGGAGTGAGTGTGTGTGCAGAGGGAG 1281
117 rThrGlyGly 120
1282 CACAGGAGGA 1291

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC81582

seq_documentation_block:

XX 07-DEC-1998; 98US-0207120.
 PR 06-JUL-1999; 99US-0142576.
 PR 21-OCT-1999; 99US-0161653.
 PR 12-NOV-1999; 99US-0165255.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 XX WPI; 2000-423420/36.
 DR P-PSDB; AAY96858.
 XX Novel zveg3 polypeptides and nucleotides encoding them useful for
 PT stimulating growth of smooth muscle cells and fibroblasts comprising an
 PT epitope bearing portion of a specific amino acid sequence
 XX
 FS Claim 29; Page 146-148; 173pp; English.
 XX This cDNA encodes a human vascular endothelial growth factor homologue,
 CC designated ZVEGF3. Polypeptides comprising an epitope-bearing portion
 CC human or murine ZVEGF3 are claimed. The growth factors comprise a growth
 CC factor domain and a CUB domain (generic sequence motifs are shown in
 CC AAY96859 and AAY96860). The growth factor domain is characterized by an
 CC arrangement of cysteine residues and beta-strands that is characteristic
 CC of the "cysteine knot" structure of the platelet-derived growth factor
 CC (PDGF) family. The CUB domain shows homology to CUB domains in
 CC neuropilins, human bone morphogenetic protein-1, porcine seminal plasma
 CC protein, bovine acidic seminal fluid protein and Xenopus laevis
 CC tollid-like protein. Structural analysis and homology predict that
 CC ZVEGF3 polypeptides complex with a second polypeptide to form multimeric
 CC proteins. The human zveg3 gene has been mapped to chromosome 4q28.3.
 CC ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth
 CC muscles cells, for activating cell surface PDGF-alpha receptor and for
 CC inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is
 CC useful for regulating (post-development) organ growth, regeneration and
 CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3
 CC antagonists are useful for treating cancer, rheumatoid arthritis,
 CC diabetic retinopathy, ischemic limb disease, peripheral vascular
 CC disease, myocardial ischemia, vascular intimal hyperplasia,
 CC atherosclerosis, wound healing, chronic liver disease and haemangioma
 CC formation. ZVEGF3 can also be used to modulate neurite growth and
 CC development of the nervous system, and for treating neurodegenerative
 CC diseases.
 XX
 SQ Sequence 1760 BP; 494 A; 373 C; 411 G; 482 T; 0 other;

alignment_scores:
 Quality: 666.00 Length: 120
 Ratio: 5.550 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_copy_226_345 x AAA51498 ..

Align seg 1/1 to: AAA51498 from: 1 to: 1760

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
 |||||
 829 GCCTTTGTTTGGAGAAAAATCCAGAGTGGTGCATCTGAACCTTCTAAC 878
 |||||
 17 rGluGlnValArgLeuTyrSerCysThrProArgAsnPheserValSerI 34
 |||||
 879 AGAGAGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTC 928
 |||||
 34 leArgGluGlnLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
 |||||
 929 TAAGGGAGAAACATAAGAGAACCATACCATTTTCTGGCCAGGTGTGCTC 978
 |||||
 51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
 |||||

979 CTGGTTAAACCGCTGGTGGGAACCTGTCCTGTTGTCTCCACAANTGCAA 1028
 |||||
 67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
 |||||
 1029 TCAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAATACACAGAGTCC 1078
 |||||
 84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
 |||||
 1079 TTCAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCACTCACC 1128
 |||||
 101 AspValAlaLeuGluHisGluGluCysAspCysValCysArgGlySe 117
 |||||
 1129 GACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAG 1178
 |||||
 117 rThrGlyGly 120
 |||||
 1179 CACAGGAGGA 1188

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT: AAD04649

seq_documentation_block:

ID AAD04649 standard; DNA; 1760 BP.

XX

AC AAD04649;

XX

DT 04-JUL-2001 (first entry)

XX

DE Human Zveg3 DNA.

XX

KW Human; Zveg3 antagonist; cell proliferation; stellate cell activation;
 KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
 KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;
 KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
 KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
 KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
 KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
 KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
 KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
 KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
 KW fibroproliferative disorder; ds.

XX Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 154..1191

FT /tag= a

FT /product= "Human Zveg3 protein"

FT sig_peptide 154..195

FT /tag= b

FT mat_peptide 196..1188

FT /tag= c

FT /product= "Mature human Zveg3 protein"

FT

XX WO200128586-A1.

XX

XX 26-APR-2001.

XX

PF 23-OCT-2000; 2000WO-US29270.

XX

PR 21-OCT-1999; 99US-0161653.

PR 12-NOV-1999; 99US-0165255.

PR 01-AUG-2000; 2000US-0222223.

XX

XX (ZYMO) ZYMOGENETICS INC.

XX

PI Gilbertson DG;

XX

DR WPI; 2001-300278/31.

DR P-PSDB; AAE00997.

XX

PT use of zveg3 antagonist for reducing fibroproliferative disorder of
 PT kidney, liver and bone, reducing extracellular matrix production,
 PT treating fibrosis or reducing stellate cell activation in mammal

XX Example 1; Page 54-56; 70pp; English.
PS The patent discloses materials and methods for reducing cell
XX proliferation or extracellular matrix production, treating fibrosis and
CC reducing stellate cell activation in a mammal. The method comprises
CC administering a composition containing a zveg3 antagonist in combination
CC with a delivery vehicle. The zveg3 is a protein that is structurally
CC related to platelet-derived growth factor (PDGF) and the vascular
CC endothelial growth factors (VEGF). The zveg3 protein is also designated
CC as "VEGF-R" and "PDGF-C". The zveg3 antagonist is useful to block the
CC mitogenic effects of zveg3 and thereby to inhibit or prevent and treat
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and
CC alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
CC fibrotic disorders of pancreas, fibroproliferative disorders of the
CC vasculature such as transplant vasculopathy and fibroproliferative
CC disorders of the bone such as osteopetrosis and hyperostosis.
XX The present sequence is human zveg3 DNA.
XX
SQ Sequence 1760 BP; 494 A; 373 C; 411 G; 482 T; 0 other;

alignment_scores:
Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-457-066-2_COPY_226_345 x AAD04649 ..
Align seg 1/1 to: AAD04649 from: 1 to: 1760

1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
829 GCITTTGTTTTTGGAGAAATCCAGAGTGGTGATCTGAACCTTCTAAC 878
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||
879 AGAGGAGGTAAAGATTATACAGCTCCACACCTCGTAACCTCTCAGTGCCA 928
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||
929 TAAGGGAAGAACTAAAGAGAACCCGATACCATTTTCTGCCAGGTTGCTC 978
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
979 CTGGTTAAACGCTGTGGTGGAACTGCGCTGTGTCTCCACAATTGCAA 1028
67 nGluCysGlnCysValProSerLysValThrLysLysThrHisGluValL 84
|||||
1029 TGAATGTCATGTGTCCTCAAGCAAGTTACTAAAAATACACAGGTC 1078
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
1079 TTCAGTTGAGACCAAGACCGGTGTCAGGCGATTGCACAAATCACTCAC 1128
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
|||||
1129 GAGCTGGCCCTGGAGCACCATTAGAGGAGTGTGACGTGTGTGCAGAGGAG 1178
117 rThrGlyGly 120
|||||
1179 CACAGGAGGA 1188

seq_name: /SID52/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA12523
seq_documentation_block:
ID AAA12523 standard; cDNA; 2108 BP.

XX AAA12523;
XX AC
XX 25-JUL-2000 (first entry)
XX cDNA encoding platelet-derived growth factor C (PDGF-C).
XX Platelet-derived growth factor C; PDGF-C; cell proliferation;
KW growth factor; heparin; connective tissue; wound healing; VEGF-F;
KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
KW lung carcinoma; erythroleukemia; tissue remodelling; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS .37..1073
XX /*tag= a
XX /product= "platelet-derived growth factor C"
XX WO200018212-A2.
XX
XX 06-APR-2000.
XX
XX 30-SEP-1999; 99WO-US22668.
XX
XX 30-SEP-1998; 98US-0102461.
XX 12-NOV-1998; 98US-0108109.
XX 03-DEC-1998; 98US-0110749.
XX 18-DEC-1998; 98US-0113002.
XX 21-MAY-1999; 99US-0135426.
XX 15-JUL-1999; 99US-0144022.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
XX Eriksson U, Aase K, Lee X, Ponten A, Untela M, Alitalo K;
XX Oestman A, Heldin C, Betscholz C;
XX
XX WPI; 2000-292954/25.
XX P-PSDB; AAY84557.
XX
XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
XX differentiation, growth and motility of cells expressing the PDGF-C
XX receptor
XX
XX Claim 9; Fig 1; 135pp; English.
XX
XX The present sequence encodes human platelet-derived growth factor C
XX (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the
XX ability to stimulate and enhance proliferation or differentiation,
XX and/or growth or motility of cells expressing a PDGF-C receptor.
XX PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
XX proliferation, preferably in combination with one other growth factor
XX and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
XX be used for stimulating connective tissue or wound healing. The
XX PDGF-C polypeptide can be enzymatically processed to generate the active
XX truncated form of PDGF-C and used to regulate the receptor-binding
XX specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
XX mitogenesis in a mammal and to induce PDGF alpha receptor activation.
XX PDGF-C antagonists can be used to inhibit tumour growth of a tumour
XX expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
XX choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
XX and erythroleukemia, can be identified by testing for expression of
XX PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
XX remodelling during invasion of tumour cells into a normal population of
XX cells. Antagonists can also be used to treat fibrotic conditions,
XX especially found in the lung, kidney or liver.
XX
XX Sequence 2108 BP; 623 A; 400 C; 451 G; 629 T; 5 other;
XX
XX alignment_scores:

Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_226_345 x AAA12523 ..
Align seg 1/1 to: AAA12523 from: 1 to: 2108

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
712 GCTTTTGGTTTGGAGAAATCCAGAGTGGTGAATCTGAACCTTCTAAC 761
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
762 ACAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGCCA 811
34 leArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeu 50
812 TAAGGAAGAAGCTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTC 861
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
862 CTGGTTAAACGCTGTGGTGAACCTGTGCTGTCTCCACCAATTGCCAA 911
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
912 TGAATGCTCAATGTGCTCCAGCAAGTACTATAAAATACACAGAGTCC 961
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
962 TTCAGTTGAGACCAAGACCGGTGTGAGGGGATTCACAAATCACTCACC 1011
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
1012 GAGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGAGAGGGAG 1061
117 rThrGlyGly 120
1062 CACAGGAGGA 1071

seq_name: /SID82/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71951

seq_documentation_block:

ID AAA71951 standard; DNA; 2475 BP.

AC AAA71951;

XX 19-JAN-2001 (first entry)

XX Human RACE generated VEGF-X DNA.

XX VEGF-X; vascular endothelial growth factor; human; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 122..1159

XX /*tag= a

XX /product= "VEGF-X"

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC) JANSSEN PHARM NV.
XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJJ, Gosiewska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI: 2000-442669/38.
DR P-PSDB; AAB10633.
XX
PT New vascular endothelial growth factor protein; useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 6; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
CC (vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence encodes the RACE generated human VEGF-X
CC protein described in the method of the invention.
XX
SQ Sequence 2475 BP; 730 A; 473 C; 523 G; 749 T; 0 other;

alignment_scores:

Quality: 666.00 Length: 120

Ratio: 5.550 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-457-066-2_COPY_226_345 x AAA71951

Align seg 1/1 to: AAA71951 from: 1 to: 2475

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17

797 GCTTTTGGTTTGGAGAAATCCAGAGTGGTGAATCTGAACCTTCTAAC 846

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34

847 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGCCA 896

34 leArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeu 50

897 TAAGGAAGAAGCTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTC 946

51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67

947 CTGGTTAAACGCTGTGGTGGGAACCTGTGCTGTCTCCACCAATTGCCAA 996

67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84

997 TGAATGCTCAATGTGCTCCCAAGCAAGTTACTAAAAAATACACAGAGTCC 1046

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100

1047 TTCAGTTGAGACCAAGACCGGTGTGAGGGGATTCACAAATCACTCACC 1096

101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117

|||||

1097 GACGTGGCCCTGGAGCACCATGAGAGTGTGACTGTGTGTGCAGAGGGAG 1146

117 rThrGlyGly 120
|||||
1147 CACAGGAGGA 1156

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71990

seq_documentation_block:
ID AAA71990 standard; cDNA; 2668 BP.

XX AC AAA71990;

XX DT 19-JAN-2001 (first entry)

XX DE Human VEGF-X cDNA.

XX KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 267..1304

XX FT /*tag= a

XX FT /product= "VEGF-X"

XX PN WO200037641-A2.

XX PD 29-JUN-2000.

XX PF 21-DEC-1999; 99WO-US30503.

XX PR 22-DEC-1998; 98GB-0028377.

XX PR 18-MAR-1999; 99US-0124967.

XX PR 08-NOV-1999; 99US-0164131.

XX PA (JANC) JANSSEN PHARM NV.

XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

XX PI Dhanaraj SN, Xu J;

XX DR WPI; 2000-442669/38.

XX DR P-PSDB; AAB10644.

XX PT New vascular endothelial growth factor protein, useful for treating or
XX PT preventing diseases associated with inappropriate angiogenesis activity
XX PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX PS Disclosure; Fig 30B; 127pp; English.

XX CC This invention describes a novel vascular endothelial growth factor-X
XX CC (VEGF-X) protein (1a) and its encoding polynucleotide (11a) which has
XX CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
XX CC antidiabetic activity and acts as an angiogenesis and vascularization
XX CC regulator. An antisense molecule of the invention is useful for treating
XX CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX CC retinopathy by inhibiting angiogenic activity or inappropriate
XX CC vascularization including formation and proliferation of new blood
XX CC vessels, growth and development of tissues, tissue regeneration and organ
XX CC and tissue repair in a subject. The products of the invention are useful
XX CC for preparing medicaments for treating wounds such as dermal ulcers,
XX CC pressure sores, venous sores, diabetic ulcers and burns and to promote
XX CC skin graft growth, tissue repair, proliferation of new blood vessels,
XX CC tissue regeneration and organ repair by promoting angiogenic activity or
XX CC vascularization. This invention encodes a human VEGF-X protein described
XX CC in the method of the invention.

XX SQ Sequence 2668 BP; 780 A; 511 C; 567 G; 810 T; 0 other;

alignment_scores:
Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-457-066-2_COPY_226_345 x AAA71990 ..
Align seg 1/1 to: AAA71990 from: 1 to: 2668
1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
942 GCTTTTGTGGGAAAGAAATCCAGAGTGGTGATCTGAACCTTCTAAC 991
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||
992 AGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCAGTGTCCA 1041
34 leArgGluGluLeuLysArgThrAspThrIlePheThrProGlyCysLeu 50
|||||
1042 TAAGGGAAGAACTAAAGAGACCGATACCATTTCTGGCCAGGTGTCTC 1091
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
1092 CTGGTTAAACGCTGTGGTGGAACTGTGCTGTCTCCACAATTGCRA 1141
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
|||||
1142 TGAATGTCAATGTCTCCCAAGCAAACTTACATAAAAAATACCACGAGTCC 1191
84 euGluLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
1192 TTCAGTTGAGACCAAGACCGGTGTTCAGGGGATTCACAAATCACATCAC 1241
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
|||||
1242 GACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAG 1291
117 rThrGlyGly 120
|||||
1292 CACAGGAGGA 1301

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA71952

seq_documentation_block:

ID AAA71952 standard; DNA; 2776 BP.

XX AC AAA71952;

XX DT 19-JAN-2001 (first entry)

XX DE Human VEGF-X homologue DNA.

XX KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
XX KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
XX KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
XX KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
XX KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX KW venous sore; diabetic ulcer; burns; skin graft growth; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 260..1297

XX FT /*tag= a

XX FT /product= "VEGF-X homologue"

XX PN WO200037641-A2.

XX PD 29-JUN-2000.

PF 21-DEC-1999; 99WO-US30503.
 XX
 XX 22-DEC-1998; 98GB-0028377.
 PR 18-MAR-1999; 99US-0124967.
 PR 08-NOV-1999; 99US-0164131.
 XX
 PA (JANC) JANSSEN PHARM NV.
 XX
 XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
 PI Dhanaraj SN, Xu J;
 XX
 DR WPI; 2000-442669/38.
 DR P-PSDB; AAB10634.
 XX
 PT New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
 XX
 XX Disclosure; Fig 7; 127pp; English.
 XX
 CC This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation and proliferation of new blood
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence encodes the human VEGF-X protein homologue
 CC described in the method of the invention.
 XX
 XX Sequence 2776 BP; 825 A; 515 C; 587 G; 849 T; 0 other;

alignment_scores:
 Quality: 666.00 Length: 120
 Ratio: 5.550 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-457-066-2_COPY_226_345 x AAA71952

Align seg 1/1 to: AAA71952 from: 1 to: 2776

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
 |||||
 935 GCTTTGTTGTTTGGAGAAATCCACAGTGGTGATCTGAACCTTCTAAC 984

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
 |||||
 985 ACAGAGAGGTAAATATACAGCTGCACCTCTGTAACCTCTCAGTGCCA 1034

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
 |||||
 1035 TAAGGAAGAACTAAAGAACCGATACCATTTCTGGCAGGTGCTC 1084

51 LeuValLysArgCysGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
 |||||
 1085 CTGGTTAAACGCTGTGGTGGGAACCTGCTGTCTCCACAATTCGAA 1134

67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluVal 84
 |||||
 1135 TGAATGTCAATGTGTCACCAAGCAAGCTTACTAAAAAATACACAGGTCC 1184

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
 |||||
 1185 TTCAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAANTCACTACC 1234

101 AspValAlaLeuGluHisGluCysAspCysValCysArgGlyse 117
 |||||
 1235 GACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAG 1284

117 rThrGlyGly 120
 |||||
 1285 CACAGGAGGA 1294

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT:AAA52458
 seq_documentation_block:
 ID AAA52458 standard; cDNA; 2779 BP.
 XX
 AC AAA52458;
 XX
 DT 25-SEP-2000 (first entry)
 XX
 XX cDNA encoding human growth factor related molecule GFRP-4.
 XX
 KW Human GFRP-4; growth factor related molecule; diseased breast tissue;
 KW bone morphogenetic protein 1; BMP-1; inflammation; immune response;
 KW reproductive tissue; reproductive tissue; developmental disorder; cell
 KW proliferative disorder; immune disorder; reproductive disorder;
 KW cardiovascular disorder; bacterial infection; viral; fungal; parasitic;
 KW cancer; allergy; asthma; arteriosclerosis; therapy; diagnosis; consensus;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 258..1295
 FT /*tag= a
 FT /product= "Human GFRP-4"
 XX
 PN WO200024774-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 28-OCT-1999; 99WO-US25458.
 XX
 PR 28-OCT-1998; 98US-0181711.
 PR 11-DEC-1998; 98US-0209547.
 PR 17-MAY-1999; 99US-0313457.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Yue H, Hillman JL, Corley NC, Guegler KJ, Baughn MR;
 PI Au-Young J;
 XX
 DR WPI; 2000-350695/30.
 DR P-PSDB; AAB03003.
 XX
 PT Human growth factor related molecule protein useful for the diagnosis
 PT and treatment of disorders associated with its activity including
 PT developmental, cell proliferative, immune, reproductive and
 PT cardiovascular disorders and infections -
 XX
 PS Claim 9; Page 76; 80pp; English.
 XX
 CC This sequence represents cDNA encoding human growth factor related
 CC molecule GFRP-4. cDNA encoding GFRP-4 was initially identified in a
 CC diseased breast tissue cDNA library, and the present sequence represents
 CC a consensus derived from several overlapping and/or extended cDNA
 CC clones. GFRP-4 has chemical and structural homology with human bone
 CC morphogenetic protein 1 (BMP-1) (27% identity at the BMP-1 C-terminus).
 CC GFRP-4 was found by Northern analysis to be expressed in reproductive
 CC and cardiovascular tissue, and in cDNA libraries associated with cancer,
 CC inflammation and the immune response. GFRP proteins (AAB03000-B03003),
 CC nucleotides encoding them (AAA52455-A52458), GFRP agonists and
 CC antagonists may be used to treat a wide variety of diseases associated
 CC with increased or decreased expression or activity of GFRP proteins.
 CC Conditions which may be treated include developmental disorders, cell

CC proliferative disorders (e.g., cancers), immune disorders (e.g., allergies, asthma), reproductive disorders (e.g., menstrual cycle disorders), cardiovascular disorders (e.g., arteriosclerosis) and CC bacterial, viral, fungal or parasitic infections. Additionally, GFRP CC proteins and nucleotides can be used in the diagnosis of such disorders.
XX
SQ Sequence 2779 BP; 832 A; 515 C; 585 G; 847 T; 0 other;

alignment_scores:
Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_226_345 x AAA52458 ..

Align seg 1/1 to: AAA52458 from: 1 to: 2779

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
933 GCITTTGTTTTGGAGAAAATCCAGAGTGGTGATCTGAACCTTCTAAC 982
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
983 AGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGCCA 1032
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
1033 TAAGGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTGTCTC 1082
51 LeuValLysArgCysGlyGlyValAsnCysAlaCysCysLeuHisAsnCysAs 67
1083 CTGTTTAAACCTGTGGTGGAACTGTCCTGTCTCCAAATGCA 1132
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
1133 TGAATGTAATGTCTCCCAAGCAAGTACTAAAAATACACAGAGTCC 1182
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
1183 TTCAGTTTGAGACCAAGACCGGTCTCAGGGGATTGCACAAATCACTACC 1232
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
1233 GACGTGGCCCTGGAGACCATGAGAGTGTGACTGTGTGTCAGAGGGAG 1282
117 rThrGlyGly 120
1283 CACAGGAGGA 1292

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ23691

seq_documentation_block:
ID AAZ23691 standard; DNA; 2825 BP.

AC AAZ23691;

DT 11-JAN-2000 (first entry)

DE Human VEGF-E DNA.

XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;
KW treatment; cardiovascular disorder; endothelial disorder; therapy;
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
KW angiogenic disorder; age-related macular degeneration; vascular disease;
KW neovascularization; tumor; gene mapping; ss.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH 259..1296
FT CDS
FT /*tag= a

FT
XX
PN WO9947677-A2. /product= "VEGF-E"
XX
PD 23-SEP-1999.
XX
XX 10-MAR-1999; 99WO-US05190.
XX
XX 17-MAR-1998; 98US-0040220.
XX 02-NOV-1998; 98US-0184216.
XX (GETH) GENENTECH INC.
XX Ferrata N, Kuo SS;
XX WPI: 1999-580306/49.
XX P-PSDB; AAY33679.
XX
XX New growth factor polypeptide useful for treating cardiovascular or
XX endothelial disorders, e.g. cardiac hypertrophy -
XX
XX Claim 2; Fig 1; 122pp; English.
XX
XX This invention describes the isolation of a novel human vascular
XX endothelial cell growth factor-E (VEGF-E) polypeptide which has
XX tranquillizer, vulnery and cardiant activity. VEGF-E can be administered
XX therapeutically, especially by expressing encoding polynucleotides, to
XX treat cardiovascular or endothelial disorders in mammals, especially
XX humans. It is useful in wound repair and tissue generation and
XX regeneration, and may especially be used to treat cardiac hypertrophy
XX It can be combined with a carrier in pharmaceutical compositions, which
XX can be administered to treat disorders as above. VEGF-E can be used to
XX screen for antagonists and agonists, and the antagonists administered to
XX treat angioenic disorders in mammals (especially humans) e.g. cancer or
XX age-related macular degeneration. It can be used to generate antibodies,
XX useful therapeutically as antagonists, as above. The antibodies are also
XX useful to detect VEGF-E polypeptide, especially to diagnose
XX cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
XX vascular disease, or neovascularization associated with tumor formation),
XX by contacting the antibody with a tissue sample and detecting formation
XX of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
XX VEGF-E can be used to diagnose cardiovascular and endothelial disorders
XX in mammals, by detecting abnormally high or low VEGF-E gene expression in
XX tissue samples. They can also be used to diagnose a disease or
XX susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
XX cardiovascular, endothelial or angiogenic disorder such as a tumor), by
XX detecting a mutation in the VEGF-E encoding sequence isolated from a
XX sample. They may also be used to produce probes useful to detect related
XX sequences or for gene mapping. This sequence encodes the human VEGF-E
XX protein described in the method of the invention.
XX
XX SQ Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;

alignment_scores:
Quality: 666.00 Length: 120
Ratio: 5.550 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-457-066-2_COPY_226_345 x AAZ23691 ..

Align seg 1/1 to: AAZ23691 from: 1 to: 2825

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
934 GCITTTGTTTTGGAGAAAATCCAGAGTGGTGATCTGAACCTTCTAAC 983
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
984 AGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTGCCA 1033
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50

|||||
1034 TAAGGGAAGAAC TAAAGAGAACCGATACCATTTCTGGCCAGGTGTCTC 1083
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
1084 CTGGTTAAACGCTGTGTGGGAACCTGTGCCTGTGTCTCCACAATTGCAA 1133
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
|||||
1134 TGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 1183
84 euGlnLeuArgProLysThrClyValArgGlyLeuHisLysSerLeuThr 100
|||||
1184 TTCAGTTGAGACCAAGACCGGTGTACAGGGGATTCACAAATCACTACC 1233
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
|||||
1234 GACGTGCCCCCTGGAGCACCACCATGAGGAGTGTGACTGTGTGTCCAGAGGAG 1283
117 rThrGlyGly 120
|||||
1284 CACAGGAGGA 1293

Search time (sec): 38.750000

/cgn2_6/ptodata/2/ina/6B.COMB.seq:US-08-915-795-7 +	119.50	236.97	1.5e-05	1135	!
/cgn2_6/ptodata/2/ina/6B.COMB.seq:US-08-915-795-6 +	119.50	235.25	1.9e-05	1325	!
/cgn2_6/ptodata/2/ina/6B.COMB.seq:US-08-915-795-4 +	115.50	221.69	0.0001	2029	!
/cgn2_6/ptodata/2/ina/6B.COMB.seq:US-08-915-795-1 +	115.50	217.93	0.0002	2846	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-989-251-4 +	112.00	233.40	2.4e-05	352	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-09-340-250-4 +	112.00	233.40	2.4e-05	352	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-867-352-24 +	108.00	218.20	0.0002	625	!
/cgn2_6/ptodata/2/ina/backfiles1.seq:5175255-3 +	108.00	217.08	0.0002	691	!
/cgn2_6/ptodata/2/ina/backfiles1.seq:519756-14 +	108.00	216.46	0.0002	731	!
/cgn2_6/ptodata/2/ina/backfiles1.seq:5219739-14 +	108.00	216.34	0.0002	739	!
/cgn2_6/ptodata/2/ina/5A.COMB.seq:US-08-387-845-3 +	108.00	214.55	0.0003	868	!
/cgn2_6/ptodata/2/ina/5B.COMB.seq:US-08-778-275-3 +	108.00	214.55	0.0003	868	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-867-352-3 +	108.00	214.55	0.0003	868	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-989-251-28 +	108.00	209.90	0.0005	1320	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-09-340-250-28 +	108.00	209.90	0.0005	1320	!
/cgn2_6/ptodata/2/ina/5A.COMB.seq:US-08-469-427A-10 +	105.50	213.70	0.0003	570	!
/cgn2_6/ptodata/2/ina/5B.COMB.seq:US-08-609-443B-10 +	105.50	213.70	0.0003	570	!
/cgn2_6/ptodata/2/ina/5B.COMB.seq:US-08-569-063C-10 +	105.50	213.70	0.0003	570	!
/cgn2_6/ptodata/2/ina/5B.COMB.seq:US-08-609-443B-14 +	105.50	212.69	0.0003	624	!
/cgn2_6/ptodata/2/ina/5B.COMB.seq:US-08-569-063C-14 +	105.50	212.69	0.0003	624	!
/cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:PCT-US93-07612-8 +	105.00	218.76	0.0002	327	!
/cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:PCT-US91-02766-17 +	105.00	218.36	0.0002	333	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-989-251-3 +	105.00	217.94	0.0002	352	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-09-340-250-3 +	105.00	217.94	0.0002	352	!
/cgn2_6/ptodata/2/ina/5A.COMB.seq:US-08-094-079-12 +	105.00	217.66	0.0002	361	!
/cgn2_6/ptodata/2/ina/5A.COMB.seq:US-08-094-079-18 +	105.00	217.66	0.0002	361	!
/cgn2_6/ptodata/2/ina/backfiles1.seq:5428135-1 +	105.00	217.01	0.0002	383	!
/cgn2_6/ptodata/2/ina/5A.COMB.seq:US-08-445-847A-2 +	105.00	216.92	0.0002	386	!
/cgn2_6/ptodata/2/ina/5B.COMB.seq:US-08-257-494D-6 +	105.00	216.92	0.0002	386	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-875-357A-5 +	105.00	216.92	0.0002	386	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-989-251-1 +	105.00	215.37	0.0002	444	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-09-340-250-1 +	105.00	215.37	0.0002	444	!
/cgn2_6/ptodata/2/ina/5A.COMB.seq:US-08-094-079-6 +	105.00	213.74	0.0003	514	!
/cgn2_6/ptodata/2/ina/5A.COMB.seq:US-08-094-079-10 +	105.00	213.74	0.0003	514	!
/cgn2_6/ptodata/2/ina/5A.COMB.seq:US-08-445-847A-3 +	105.00	212.25	0.0004	588	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-989-251-26 +	105.00	211.64	0.0004	621	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-09-340-250-26 +	105.00	211.64	0.0004	621	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-989-251-24 +	105.00	199.56	0.0018	1845	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-09-340-250-24 +	105.00	199.56	0.0018	1845	!
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-989-251-36 +	105.00	198.53	0.0021	2023	!


```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
; US-08-915-795-4

alignment_scores:
  Quality: 115.50      Length: 103
  Ratio: 1.925        Gaps: 5
  Percent Similarity: 58.252  Percent Identity: 33.010

alignment_block:
US-09-457-066-2_COPY_226_345 x US-08-915-795-4 ..
Align seg 1/1 to: US-08-915-795-4 from: 1 to: 2029

13 LeuAsnLeuLeuThrGluGluValArgLeuTyrSerCysThrProArgAs 29
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
705 CTAAAGTTATAGATGAAGAACTGCGGGAAGAGTACCAACACATCT 754

29 nPheSerValSerIleArgGluLeu...LysArgThrAspThrIleP 45
: |||:|||||: |||: |||: |||: |||: |||: |||: |||:
755 AACGTGCGTGGAGTGGCCAGTGCAGTGGGGAAGAGTACCAACACATCT 804

45 heTrpProGlyCysLeuValLysArgCysGlyGlyAsnCysAlaCys 61
|| || ||| |||: ||| ||| ||| ||| ||| ||| ||| |||
805 TCAAGCCCTTGTGTGAACGTGTTCGATGTGTGGTGC.....TGT 845

62 CysLeuHisAsnCysAsnGluCys...GlnCysValProSerLysValTh 77
||| |||:|||||: |||: |||: |||: |||: |||: |||: |||:
846 TCCAATGAAGAGAGCCTTATCTGTATGAACACAGCACCCTCGACATTC 895

77 rLysLysTyrHisGluValLeuGlnLeuArgProLysThrGlyValArg 94
|||||: |||: |||: |||: |||: |||: |||: |||: |||:
896 CAACAGCTCTTTGAGATATCAGTG.....CCTTTGACATCAGTA.... 935

94 lyLeuHisLysSerLeuThrAspValAlaLeuGluHisGluGluCys 110
: |||: |||: |||: |||: |||: |||: |||: |||: |||:
936 .....CCTGAATTAGTGCCTGTTAAAGTTGCCAATCATACAGGTGT 977

111 AspCysVal 113
|||||:
978 AAGTGCCTTG 986

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-915-795-1

seq_documentation_block:
; Sequence 1, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Karl ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2846 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Breast
; US-08-915-795-1

alignment_scores:
  Quality: 115.50      Length: 103
  Ratio: 1.925        Gaps: 5
  Percent Similarity: 58.252  Percent Identity: 33.010

alignment_block:
US-09-457-066-2_COPY_226_345 x US-08-915-795-1 ..
Align seg 1/1 to: US-08-915-795-1 from: 1 to: 2846

13 LeuAsnLeuLeuThrGluGluValArgLeuTyrSerCysThrProArgAs 29
|||||:|||||: |||: |||: |||: |||: |||: |||: |||:
1978 CTAAAGTTATAGATGAAGAACTGCGGGAAGAGTACCAACACATCT 2027

29 nPheSerValSerIleArgGluLeu...LysArgThrAspThrIleP 45
: |||:|||||: |||: |||: |||: |||: |||: |||: |||:
2028 AACGTGCGTGGAGTGGCCAGTGCAGTGGGGAAGAGTACCAACACATCT 2077

45 heTrpProGlyCysLeuValLysArgCysGlyGlyAsnCysAlaCys 61
|| || ||| |||: ||| ||| ||| ||| ||| ||| ||| |||
2078 TCAAGCCCTTGTGTGAACGTGTTCGATGTGTGGTGC.....TGT 2118

62 CysLeuHisAsnCysAsnGluCys...GlnCysValProSerLysValTh 77
||| |||:|||||: |||: |||: |||: |||: |||: |||: |||:
2119 TGCAATGAAGAGAGCCTTATCTGTATGAACACAGCACCCTCGTACATTC 2168

77 rLysLysTyrHisGluValLeuGlnLeuArgProLysThrGlyValArg 94
|||||: |||: |||: |||: |||: |||: |||: |||: |||:
2169 CAACAGCTCTTTGAGATATCAGTG.....CCTTTGACATCAGTA.... 2208

94 lyLeuHisLysSerLeuThrAspValAlaLeuGluHisGluGluCys 110
: |||: |||: |||: |||: |||: |||: |||: |||: |||:
2209 .....CCTGAATTAGTGCCTGTTAAAGTTGCCAATCATACAGGTGT 2250

111 AspCysVal 113
|||||:
2251 AAGTGCCTTG 2259

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-989-251-4

seq_documentation_block:
; Sequence 4, Application US/08989251
; Patent No. 6017731
; GENERAL INFORMATION:
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN YEAST
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,251
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5784-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Complementing strand to the
DESCRIPTION: preceding SEQ ID NO:, listed to show the terminal overhangs
DESCRIPTION: produced upon assembly."
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-989-251-4

alignment_scores:
Quality: 112.00 Length: 107
Ratio: 1.867 Gaps: 8
Percent Similarity: 56.075 Percent Identity: 33.645

alignment_block:

US-09-457-066-2_COPY_226_345 x US-08-989-251-4/rev ..

Align seg 1/1 to reverse of: US-08-989-251-4 from: 1 to: 352

16 LeuThrGluGluValArgLeuTyrSerCysThrProArg...AsnPheSe 31
324 ATCGCTGAACCAAGCTATGATCGCTGATGTAAGACTAGAACTAGTTTC 275
31 rValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....T 46
274 GAAATCTCCAGAAGATTTCGATCGACAGAACTAACGCTAAGTTCTTGTTT 225
46 rpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCys 62
224 GCCCACCATTGTGTGAAGTTCAAAGATGTTCTGGT.....TGTTGT 184
63 LeuHisAsnCysAsnGlnCysGlnCysValProSerLysValThrLysLy 79
183AACACAGAAAGCTTCAATGATAGACCAACTCAAGT..... 148
79 styHisGluValLeuGlnLeuArgPro.....LysThrGlyV 92
147CAATGACACAGTTCAAGTTAGAAAGATCGAAA 114
92 al.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGlu 105
113 TCGTTAGAAAGAACCAATCTTCAAGAAGGCTACT...GTACTTTGGAA 67
106 HisHisGluGluCysAspCys 112
||| ||| |||

66 GACCACCTGGCTTGTAAGTGT 46
seq_name: /cgn2_5/ptodata/2/ina/6A_COMB.seq:US-09-340-250-4
seq_documentation_block:
Sequence 4, Application US/09340250
Patent No. 6083723
GENERAL INFORMATION:
APPLICANT: Tekamp-Olson, Patricia
TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
TITLE OF INVENTION: PROTEINS IN YEAST
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
STREET: 3605 Glenwood Ave. Suite 310
CITY: Raleigh
STATE: NC
COUNTRY: US
ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,250
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,251
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5784-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Complementing strand to the
DESCRIPTION: preceding SEQ ID NO:, listed to show the terminal overhangs
DESCRIPTION: produced upon assembly."
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-340-250-4

alignment_scores:
Quality: 112.00 Length: 107
Ratio: 1.867 Gaps: 8
Percent Similarity: 56.075 Percent Identity: 33.645

alignment_block:

US-09-457-066-2_COPY_226_345 x US-09-340-250-4/rev ..

Align seg 1/1 to reverse of: US-09-340-250-4 from: 1 to: 352

16 LeuThrGluGluValArgLeuTyrSerCysThrProArg...AsnPheSe 31
324 ATCGCTGAACCAAGCTATGATCGCTGATGTAAGACTAGAACTAGTTTC 275
31 rValSerIleArgGluGluLeuLysArgThrAspThrIlePhe.....T 46
274 GAAATCTCCAGAAGATTTCGATCGACAGAACTAACGCTAAGTTCTTGTTT 225
46 rpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCys 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

224 GGCCACCATGTGTGAAGTTCAAGATGTTCTGGT .....TGTTGT 184
63 LeuHisAsnCysAsnGluCysGlnCysValProSerLysValThrLysLy 79
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
183 .....AACACAGAACGTTCAATGTAGACCAACTCAAGTT ..... 148
79 sTyvHisGluValLeuGlnLeuArgPro.....LysThrGlyV 92
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
147 .....CAATTGAGACCAAGTTCAAGTTAGAAAGATCGAAA 114
92 al.....ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGlu 105
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
113 TCCTTAGAAGACCAATCTTCAGAGAGGCTACT...GTACTTTGGAA 67
106 HisHisGluGluCysAspCys 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 GACCACCTGGCTGTGAAGTGT 46

```

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-867-352-24

```

seq_documentation_block:
; Sequence 24, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multicistronic expression units and their use
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,352
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,847
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: pSBC-1/-2-PDGF-B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..609
; OTHER INFORMATION: /product= "PDGF-B
; OTHER INFORMATION: precursor sequence"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 283..609
; OTHER INFORMATION: /product= "mature PDGF-B chain"
; US-08-867-352-24

```

```

alignment_scores:
  Quality: 108.00      Length: 121
  Ratio: 1.636        Gaps: 11
  Percent Similarity: 54.545      Percent Identity: 34.711

```

```

alignment_block:
US-09-457-066-2_COPY_226_345 x US-08-867-352-24

```

Align seg 1/1 to: US-08-867-352-24 from: 1 to: 625

5 GlyArgLysSerArgValValAspLeuLeuLeuThr.....GluGl 19

```

274 GGAGAAGAGAGC.....CTGGGTTCCCTGACCATTGCTGAGCC 311
19 uValArgLeuTyvSerCysThrProArgAsn.....PheSerValSerI 34
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
312 GGCCATGATCGCGGAGTGCAAGACGCGCACGAGGTGTTTCGAGATCTCC. 360
34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
361 ..CGCGCGCTCATAGACCGCACCACTTCTGGTGTGGCGCGCC 408
49 CysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHis 65
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
409 TGTGTGGAGGTGCGCGCTGCTCCGGC.....TGCTGC.....AA 443
65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyvHis 82
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
444 CNAACGCAACGTGCAGTGCGCGCCACCCAGGTG..... 477
82 luValLeuGlnLeuArgPro.....LysThrGlyVal..... 92
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
478 .....CAGCTGCGACCTGTCCAGGTGAGAAAGATCGAGATTGCGG 519
93 ...ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisGl 108
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
520 AAGAAGCCCAATCTTTAAGAAGGCCACG...GTACGCTGGAAGACCACCT 566
108 uGluCysAspCys 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
567 GGCATGCAAGTGT 579

```

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5175255-3

```

seq_documentation_block:
; Patent No. 5175255
; APPLICANT: Thomson, Arlen R.; Nicholson, Margery
; TITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
; DERIVED GROWTH FACTOR
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/06/25,344
; FILING DATE: 23-MAR-1987
; SEQ ID NO:3
; LENGTH: 691
; 5175255-3

```

```

alignment_scores:
  Quality: 108.00      Length: 121
  Ratio: 1.636        Gaps: 11
  Percent Similarity: 54.545      Percent Identity: 34.711

```

alignment_block:

US-09-457-066-2_COPY_226_345 x 5175255-3

Align seg 1/1 to: 5175255-3 from: 1 to: 691

```

5 GlyArgLysSerArgValValAspLeuLeuLeuLeuThr.....GluGl 19
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
172 GGAGAAGAGC.....CTGGGTTCCCTGACCATTGCTGAGCC 209

```

```

19 uValArgLeuTyvSerCysThrProArgAsn.....PheSerValSerI 34
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
210 GGCCATGATCGCGGAGTGCAAGACGCGCACGAGGTGTTTCGAGATCTCC. 258

```

```

34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
259 ..CGCGCGCTCATAGACCGCACCACTTCTGGTGTGGCGCGCC 306

```

```

49 CysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHis 65
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
307 TGTGTGGAGGTGCGCGCTGCTCCGGC.....TGCTGC.....AA 341

```



```
65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
| : : : : : ||||| : : : : :
342 CAACCGCAAGTCAGTGCCTGCCGCCACCCAGGTG..... 375
82 luValLeuGlnLeuArgPro.....LysThrGlyVal..... 92
| : : : : : ||||| ||||| : : : : :
376 .....CAGCTGGGACCTGTCAGGTGAGAAAGATCGAGATTGTGCGG 417
93 ...ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisG1 108
: : : : : ||||| : : : : : |||||
418 AAGAAGCCAATCTTTAAGAGGCCACG...GTGACGCTGGAAGACCACCT 464
108 uGluCysAspCys 112
||| |||
465 GGCATGCAAGTGT 477

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5194596-14

seq_documentation_block:
; Patent No. 5194596
; APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,
; C.; MITCHELL, RICHARD L.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
; GROWTH FACTOR
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/450,883
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 387,545
; FILING DATE: 27-JUL-1989
; SEQ ID NO:14:
; LENGTH: 671
5194596-14
```

```
alignment_scores:
  Quality: 108.00      Length: 121
  Ratio: 1.636        Gaps: 11
  Percent Similarity: 54.545      Percent Identity: 34.711

alignment_block:
US-09-457-066-2_COPY_226_345 x 5194596-14 ..

Align seg 1/1 to: 5194596-14 from: 1 to: 731

5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThr.....GluG1 19
||||| : : : : : |||||
235 GGAAGAAGGAGC.....CTGGGTCCCTGACCATTTGCTGAGCC 272

19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI 34
: : : : : ||||| : : : : :
273 GGCCATGATCGCGAGTGCAGACGCGCACCGAGGTGTCGAGATCTCC. 321

34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
||| : : : : : ||||| : : : : :
322 ..CGGCGCTCATAGACCGACCAACCCAACTTCCTGGTGTGCCGCC 369

49 CysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAs 65
||| : : : : : ||||| : : : : :
370 TGTGTGAGGTGCAGCGCTGCTCCGCG.....TGCTGC.....AA 404

65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
| : : : : : ||||| : : : : :
405 CAACCGCAAGTCAGTGCCTGCCGCCACCCAGGTG..... 438
82 luValLeuGlnLeuArgPro.....LysThrGlyVal..... 92
||||| |||||
439 .....CAGCTGGGACCTGTCAGGTGAGAAAGATCGAGATTGTGCGG 480

93 ...ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisG1 108
: : : : : ||||| : : : : : |||||
481 AAGAAGCCAATCTTTAAGAGGCCACG...GTGACGCTGGAAGACCACCT 527
```

```
108 uGluCysAspCys 112
||| |||
528 GGCATGCAAGTGT 540

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5219739-14

seq_documentation_block:
; Patent No. 5219739
; APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,
; JOHN C.; MITCHELL, RICHARD L.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING BVGEF120 AND
; BVGEF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN
; VASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVGEF120 AND BVGEF121
; NUMBER OF SEQUENCES: 40
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/559,041
; FILING DATE: 27-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 450,883
; FILING DATE: 14-DEC-1989
; APPLICATION NUMBER: 387,545
; FILING DATE: 27-JUL-1989
; SEQ ID NO:14:
; LENGTH: 739
5219739-14

alignment_scores:
  Quality: 108.00      Length: 121
  Ratio: 1.636        Gaps: 11
  Percent Similarity: 54.545      Percent Identity: 34.711

alignment_block:
US-09-457-066-2_COPY_226_345 x 5219739-14 ..

Align seg 1/1 to: 5219739-14 from: 1 to: 739

5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThr.....GluG1 19
||||| : : : : : |||||
243 GGAAGAAGGAGC.....CTGGGTCCCTGACCATTTGCTGAGCC 280

19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI 34
: : : : : ||||| : : : : :
281 GGCCATGATCGCGAGTGCAGACGCGCACCGAGGTGTCGAGATCTCC. 329

34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
||| : : : : : ||||| : : : : :
330 ..CGGCGCTCATAGACCGCACCAACCCAACTTCCTGGTGTGCCGCC 377

49 CysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAs 65
||| : : : : : ||||| : : : : :
378 TGTGTGAGGTGCAGCGCTGCTCCGCG.....TGCTGC.....AA 412

65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
| : : : : : ||||| : : : : :
413 CAACCGCAAGTCAGTGCCTGCCGCCACCCAGGTG..... 446
82 luValLeuGlnLeuArgPro.....LysThrGlyVal..... 92
||||| |||||
447 .....CAGCTGGGACCTGTCAGGTGAGAAAGATCGAGATTGTGCGG 488

93 ...ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisG1 108
: : : : : ||||| : : : : : |||||
489 AAGAAGCCAATCTTTAAGAGGCCACG...GTGACGCTGGAAGACCACCT 535

108 uGluCysAspCys 112
||| |||
536 GGCATGCAAGTGT 548

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-387-845-3

seq_documentation_block:
```

```

49 CysLeuLeuValLysArgCysGlyAlaCysCysLeuHisAs 65
||||: |||:|||||:||||
409 TGTGTGGAGTGCAGCGCTGCTCCGCGC.....TGCTGC.....AA 443

65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
| :|||: |||:|||||:|||||
444 CAACCGCAACGTGCAGTGCAGCGCCGCCACCCAGGTG..... 477

82 luValLeuGlnLeuArgPro.....LysThrGlyVal..... 92
|||||:|||||:|||||
478 .....CAGTGCAGACCTGTCAGCGTGAGAAAGATCGAGATTGTCGGG 519

93 ...ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisHisG 108
||: ||: |||: |||:|||||:||||
520 AAGAAGCAACATCTTTAAGAGGCCACG...GTGCGCTGGAAGACCACCT 566

108 uGluCysAspCys 112
||| |||
567 GGCATGCAAGTGT 579

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-778-275-3

seq_documentation_block:
; Sequence 3, Application US/08778275
; Patent No. 5935819
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
; TITLE OF INVENTION: bicistronic vector system in mammalian cells
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,275
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,845
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: PMVW-2 (Weich et al., 1986)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..762
; OTHER INFORMATION: /product= "PDGF-B"
; OTHER INFORMATION: precursor sequence"
; OTHER INFORMATION: /note= "human PDGF-B gene from pGEN2-PDGF-B
; OTHER INFORMATION: flanked by 5'-EcoRI und 3'-HindIII
; OTHER INFORMATION: restriction cleavage sites"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 283..609
; OTHER INFORMATION: /product= "mature PDGF-B chain"
; PUBLIC INFORMATION:
; AUTHORS: Weich, H. A.
; AUTHORS: Seibald, W.
; AUTHORS: Schairer, H. U.
; AUTHORS: Hoppe, U.
; JOURNAL: FEBS Lett.
; VOLUME: 198
; PAGES: 344-348

```

```

? ORGANISM: Homo sapiens
? IMMEDIATE SOURCE:
? CLONE: pmwv-2 (Weich et al., 1986)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 40..762
? OTHER INFORMATION: /product= "PDGF-B
? OTHER INFORMATION: precursor sequence"
? OTHER INFORMATION: /note= "human PDGF-B gene from pGEM2-PDGF-B
? OTHER INFORMATION: flanked by 5'-EcoRI and 3'-HindIII
? OTHER INFORMATION: restriction cleavage sites"
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 283..609
? OTHER INFORMATION: /product= "mature PDGF-B chain"
? PUBLICATION INFORMATION:
? AUTHORS: Weich, H. A.
? AUTHORS: Seibald, W.
? AUTHORS: Schairer, H. U.
? AUTHORS: Hoppe, U.
? JOURNAL: FEBS Lett.
? VOLUME: 198
? PAGES: 344-348

```

DATE: 1986
US-08-778-275-3

alignment_scores:
Quality: 108.00 Length: 121
Ratio: 1.636 Gaps: 11
Percent Similarity: 54.545 Percent Identity: 34.711

alignment_block:

US-09-457-066-2_COPY_226_345 x US-08-778-275-3 ..

Align seg 1/1 to: US-08-778-275-3 from: 1 to: 868

```
5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThr.....GluG1 19
|||||:|||||
274 GGAAGAAGGAGC.....CTGGTTCCCTGACCATGCTGAGCC 311
|||:|:|:|:|:|:|
19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI 34
|||:|:|:|:|:|:|
312 GGCCATGATCGCCGAGTGCAGACGCGCACCGAGGTGTTCCGAGATCTCC. 360
|||:|:|:|:|:|:|
34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
|||||:|:|:|:|:|:|
361 ..CGGCGCCTCATAGACCGCACCAACGCAACTTCTGTGTGGCGGCC 408
|||||:|:|:|:|:|:|
49 CysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAs 65
|||||:|:|:|:|:|:|
409 TGTGTGAGGTGCAGCGCTGCTCGGC.....TGCTGC.....AA 443
|||||:|:|:|:|:|:|
65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
|||:|:|:|:|:|:|
444 CAACCGCAAGTGCAGTGCAGCGCCGCCACCCAGGTG..... 477
|||||:|:|:|:|:|:|
82 luValLeuGlnLeuArgPro.....LysThrGlyVal..... 92
|||||:|:|:|:|:|:|
478 .....CAGCTGCGACCTGTCAGGTGAGAAAGATCGAGATTGTGGCG 519
|||||:|:|:|:|:|:|
93 ...ArgGlyLeuHisSerLeuThrAspValAlaLeuGluHisG1 108
|||:|:|:|:|:|:|
520 AAGAAGCAATCTTTAAGAAGGCGACG...GTGACGCTGGAAGACCACT 566
|||||:|:|:|:|:|:|
108 uGluCysAspCys 112
|||:|:|:|:|:|:|
567 GGCATGCAAGTGT 579
```

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-867-352-3

seq_documentation_block:

Sequence 3, Application US/08867352

Patent No. 6060273

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Multicistronic expression units and their use

NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPA)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/867,352

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/387,847

FILING DATE:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 868 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PMW-2 (Weich et al., 1986)
FEATURE:
NAME/KEY: CDS
LOCATION: 40..762
OTHER INFORMATION: /product= "PDGF-B
OTHER INFORMATION: precursor sequence"
OTHER INFORMATION: /note= "human PDGF-B gene from pGEM2-PDGF-B,
OTHER INFORMATION: flanked by 5'-EcoRI und 3'-HindIII
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 283..609
OTHER INFORMATION: /product= "mature PDGF-B chain"
PUBLICATION INFORMATION:
AUTHORS: Weich, H. A.
AUTHORS: Seibald, W.
AUTHORS: Schairer, H. U.
AUTHORS: Hoppe, U.
JOURNAL: FEBS Lett.
VOLUME: 198
PAGES: 344-348
DATE: 1986
US-08-867-352-3

alignment_scores:

Quality: 108.00 Length: 121

Ratio: 1.636 Gaps: 11

Percent Similarity: 54.545 Percent Identity: 34.711

alignment_block:

US-09-457-066-2_COPY_226_345 x US-08-867-352-3 ..

Align seg 1/1 to: US-08-867-352-3 from: 1 to: 868

```
5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThr.....GluG1 19
|||||:|||||
274 GGAAGAAGGAGC.....CTGGTTCCCTGACCATGCTGAGCC 311
|||:|:|:|:|:|:|
19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI 34
|||:|:|:|:|:|:|
312 GGCCATGATCGCCGAGTGCAGACGCGCACCGAGGTGTTCCGAGATCTCC. 360
|||:|:|:|:|:|:|
34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
|||||:|:|:|:|:|:|
361 ..CGGCGCCTCATAGACCGCACCAACGCAACTTCTGTGTGGCGGCC 408
|||||:|:|:|:|:|:|
49 CysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAs 65
|||||:|:|:|:|:|:|
409 TGTGTGAGGTGCAGCGCTGCTCGGC.....TGCTGC.....AA 443
|||||:|:|:|:|:|:|
65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
|||:|:|:|:|:|:|
444 CAACCGCAAGTGCAGTGCAGCGCCGCCACCCAGGTG..... 477
|||||:|:|:|:|:|:|
82 luValLeuGlnLeuArgPro.....LysThrGlyVal..... 92
|||||:|:|:|:|:|:|
478 .....CAGCTGCGACCTGTCAGGTGAGAAAGATCGAGATTGTGGCG 519
|||||:|:|:|:|:|:|
93 ...ArgGlyLeuHisSerLeuThrAspValAlaLeuGluHisG1 108
|||:|:|:|:|:|:|
520 AAGAAGCAATCTTTAAGAAGGCGACG...GTGACGCTGGAAGACCACT 566
|||||:|:|:|:|:|:|
108 uGluCysAspCys 112
|||:|:|:|:|:|:|
567 GGCATGCAAGTGT 579
```

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-989-251-28

```

seq_documentation_block:
; Sequence 28, Application US/08989251
; Patent No. 6017731
; GENERAL INFORMATION:
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN YEAST
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,251
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5784-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic chimera"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens/Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 454..1179
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 454..519
; OTHER INFORMATION: /product= "PDGF-B prepeptide"
; OTHER INFORMATION: /standard_name= "PDGF-B presequence"
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: 455..696
; OTHER INFORMATION: /function= "mediates protein
; OTHER INFORMATION: transport"
; OTHER INFORMATION: /product= "PDGF-B prepeptide"
; OTHER INFORMATION: /standard_name= "PDGF-B presequence"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 697..1023
; OTHER INFORMATION: /product= "rhPDGF-B peptide"
; OTHER INFORMATION: /standard_name= "rhPDGF-B"
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: 1024..1179
; OTHER INFORMATION: /function= "mediates protein
; OTHER INFORMATION: transport"
; OTHER INFORMATION: /product= "PDGF-B prepeptide"
; OTHER INFORMATION: /standard_name= "PDGF-B presequence"
US-08-989-251-28

```

```

alignment_scores:
Quality: 108.00      Length: 121

```

```

Ratio: 1.636      Gaps: 11
Percent Similarity: 54.545      Percent Identity: 34.711
alignment_block:
US-09-457-066-2_COPY_226_345 x US-08-989-251-28
Align seg 1/1 to: US-08-989-251-28 from: 1 to: 1320
5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThr.....GluG1 19
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
688 GGAAGAAGAGG.....CTGGGTTCCCTGACCATTCGTGAGCC 725
19 uValArgLeuTyrSerCysThrProArgAsn.....PheSerValSerI 34
::: :::::|||||:|||||:|||||:|||||:|||||:|||||
726 GGCCATGATCGCGGAGTGCAAGACGCGCACCAGGTTGTCGAGATCTCC. 774
34 leArgGluGluLeuLysArgThrAspThrIlePhe.....TrpProGly 48
|||||: :::::|||||:|||||:|||||:|||||:|||||:|||||
775 ..CGCGGCTCATAGACGCGCACCAACGCACTCTCGTGTGTGGCGGCC 822
49 CysLeuLeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAs 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
823 TGTGTGGAGGTGCAGCGCTGCTCCGGC.....TGCTGC.....AA 857
65 nCysAsnGluCysGlnCysValProSerLysValThrLysLysTyrHisG 82
|: :::::|||||:|||||:|||||:|||||:|||||:|||||
858 CAACCGCAACGTCAGTGCCTGCCGCCGCCACCAGGTG..... 891
82 luValLeuGlnLeuArgPro.....LysThrGlyVal..... 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||
892 .....CAGCTGCGACCTGTCCAGTGAGAAAGATCGAGATTGTGCGG 933
93 ...ArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisG1 108
::: :::::|||||:|||||:|||||:|||||:|||||:|||||
934 AAGAAGCCAATCTTTAAGAAGGCCACG...GTGACGTGGAAGACCACT 980
108 uGluCysAspCys 112
||| |||
981 GCATGCAAGTGT 993
seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-340-250-28
seq_documentation_block:
; Sequence 28, Application US/09340250
; Patent No. 6083723
; GENERAL INFORMATION:
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS IN YEAST
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP
; STREET: 3605 Glenwood Ave. Suite 310
; CITY: Raleigh
; STATE: NC
; COUNTRY: US
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,250
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/989,251
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5784-4

```


Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	114.5	17.2	148	2	D49530	16K vascular endothelial
2	110	16.5	166	2	JN0248	platelet-derived growth factor
3	110	16.5	198	2	JS0735	platelet-derived growth factor
4	108	16.2	241	1	PFHUG2	platelet-derived growth factor
5	106	15.9	200	2	IS1551	platelet-derived growth factor
6	106	15.9	215	2	S08220	platelet-derived growth factor
7	106	15.9	226	2	IS1550	platelet-derived growth factor
8	105	15.8	245	1	TVC7SS	platelet-derived growth factor
9	104.5	15.7	232	2	A41551	vascular endothelial
10	104	15.6	196	2	B28964	platelet-derived growth factor
11	104	15.6	197	2	S25096	platelet-derived growth factor
12	104	15.6	211	1	PFHUG1	platelet-derived growth factor
13	104	15.6	226	1	TVMWSS	PDGF-related transmembrane
14	102.5	15.4	133	2	B49530	vascular endothelial
15	102.5	15.4	190	2	S52130	vascular endothelial
16	102.5	15.4	196	2	A37359	platelet-derived growth factor
17	102.5	15.4	196	2	A48851	platelet-derived growth factor
18	102.5	15.4	419	2	S69207	vascular endothelial
19	101.5	15.2	120	2	A33787	vascular endothelial
20	101.5	15.2	146	2	S57956	ovine vascular endothelial
21	101.5	15.2	190	2	B40080	vascular endothelial
22	97	14.6	188	2	JC4680	vascular endothelial
23	97	14.6	207	2	JC4679	vascular endothelial
24	96.5	14.5	190	2	A35987	glioma-derived vascular
25	95.5	14.3	190	2	B44881	vascular endothelial
26	95.5	14.3	214	2	A44881	vascular endothelial
27	94	14.1	225	2	S25097	platelet-derived growth factor
28	94	14.1	271	1	PFMSGB	platelet-derived growth factor
29	88	13.2	241	2	A25669	PDGF-related transmembrane

A;Cross-references: GB:M2338; NID:g214650; PIDN:AAA9928.1; PID:g214651
C;Superfamily: platelet-derived growth factor

Query Match 15.9%; Score 106; DB 2; Length 200;
Best Local Similarity 30.6%; Pred. No. 0.0026;
Matches 38; Conservative 15; Mismatches 39; Indels 32; Gaps 9;

Qy 6 RKSRYVDNLNLTETVRLYSCTPRNFVSII-REELKRTDTIF--WPGCLLVKRCGGNCACC 62
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 88 RRKRSV-----EEAVPAICKTRTVIYEIPRSQIDPISANFLIWPPCVVKRCTG---CC 138
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 63 LHNCNEQCVPSCVTKKYH-----EVLQLRPKTCVGRGLHKSLTDVALEHHHEECDCVC 114
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 139 --NTSSVKCPQSRI---HHRSVKVAKVEYVRKKPK-----LKEVL--VRLEEHLCTCTA 186
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 115 RGST 118
:
Db 187 NSNS 190
:

RESULT 6
S08220
platelet-derived growth factor chain A precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C;Accession: S08220
R;Bejcek, B.E.; Li, D.Y.; Deuel, T.F.
Nucleic Acids Res. 18, 680, 1990
A;Title: Nucleotide sequence of a cDNA clone of Xenopus platelet-derived growth factor
A;Reference number: S08220; MUID:90175018
A;Accession: S08220
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-215 <BEJ>
A;Cross-references: EMBL:X17545; NID:g64973; PIDN:CAA35583.1; PID:g64974
C;Superfamily: platelet-derived growth factor
C;Keywords: alternative splicing; growth factor
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-91/Domain: propeptide #status predicted <PRO>
F;92-215/Product: platelet-derived growth factor chain A #status predicted <MAT>

Query Match 15.9%; Score 106; DB 2; Length 215;
Best Local Similarity 30.6%; Pred. No. 0.0028;
Matches 38; Conservative 15; Mismatches 39; Indels 32; Gaps 9;

Qy 6 RKSRYVDNLNLTETVRLYSCTPRNFVSII-REELKRTDTIF--WPGCLLVKRCGGNCACC 62
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 88 RRKRSV-----EEAVPAICKTRTVIYEIPRSQIDPISANFLIWPPCVVKRCTG---CC 138
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 63 LHNCNEQCVPSCVTKKYH-----EVLQLRPKTCVGRGLHKSLTDVALEHHHEECDCVC 114
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 139 --NTSSVKCPQSRI---HHRSVKVAKVEYVRKKPK-----LKEVL--VRLEEHLCTCTA 186
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 115 RGST 118
:
Db 187 NSNS 190
:

RESULT 7
I51550
platelet-derived growth factor A chain long form precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I51550
R;Mercolla, M.; Melton, D.A.; Stiles, C.D.
Science 241, 1223-1225, 1988
A;Title: Platelet-derived growth factor A chain is maternally encoded in Xenopus embri
A;Reference number: I51550; MUID:88321676
A;Accession: I51550
A;Status: preliminary;
A;Molecule type: mRNA
A;Translated from GB/EMBL/DDBJ

A:Residues: 1-226 <MER>
A:Cross-references: GB:M2337; NID:g214648; PIDN:AAA49927.1; PTD:g214649
C:Superfamily: platelet-derived growth factor

Query Match 15.9%; Score 106; DB 2; Length 226;
Best Local Similarity 30.6%; Pred. No. 0.0029;
Matches 38; Conservative 15; Mismatches 39; Indels 32; Gaps 9;

Qy 6 R KSRVDLNLLEEYRLYSCTPRNFVSI-REELKRTDTIF--WPGCLLVKRCGGNCACC 62
| : | | || | | | | : | : | | : | | | | |
Db 88 RKRSV-----EAVPAICKTRTVIPIRSQLDPTSANFLWPCCVEVKRCTG---CC 138

Qy	63 LHNCECQCVPKVKYH-----EVLQRPKTGVRLGHLKSLTDVALEHHEDCV	114
	: :: :	
	: :: :	
Db	139 --NTSSVCKQPSRI---HHRSVKVAKVEYVRKKPK-----LKEVL--VRLEEHELECTCTA	186

Qy 115 RGST 118
::
Db 187 NSNS 190

RESULT 8
TVC1SS
platelet-derived growth factor chain B precursor - cat
N;Alternate names: PDGF-related transforming protein
C;Species: Felis silvestris catus (domestic cat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Mar-1996
C;Accession: A26402
R;Van den Ouweland, A.M.W.; Van Groningen, J.J.M.; Schalken, J.A.; Van Neck, H.W.; Bloem
Nucleic Acids Res. 15, 959-970, 1987
A;Title: Genetic organization of the c-sis transcription unit.
A;Reference number: A36402; MUID:87146463

A;Accession: A26402
A;Molecule type: mRNA
A;Residues: 1-245 <VAN>
C;Genetics:
A;Gene: sis
C;Superfamily: platelet-derived growth factor
C;Keywords: glycoprotein; growth factor; platelet; proto-oncogene; transforming protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-81/Domain: propeptide #status predicted <PRO>
F;82-194/Product: platelet-derived growth factor chain B #status predicted <MAT>
F;163-167/Region: receptor binding #status predicted
F;63/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.8%; Score 105; DB 1; Length 245;
Best Local Similarity 33.0%; Pred. No. 0.0039;
Matches 35; Conservative 13; Mismatches 36; Indels 22; Gaps 8;

QY 16 LTEEVRVLYSCTPRN--FSYSIREELKRTDTIF-WPGCLLVKRCGGNCACCLHNCNECQC 71
:
Dd 92 VAEPAMIAEKTETEVFEVS-RLIDRTNANFLVPKPCVEVORCSG---CC-NNRNVOC 145

Qy 72 VPSKVTKKY-----HEVLQRPKTGVRGLHKSLTDVALEHHEECDC 112
 |::| : |::| : | | | | | | |
 Db 146 RPTQVQLRLVQVRKIEIVRKRP-----VEKKAT-VTLEDHLACKC 184

RESULT 9
A41551
vascular endothelial growth factor 206 precursor - human
N:Alternate names: vascular permeability factor
N:Contains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VEGF
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C:Accession: A41551; C41551; A40454; B40454; C40454; A40079; A40080; JQ1463; JQ1463;
R:Bouck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.
Mol. Endocrinol. 5, 1806-1814, 1991
A:Title: The vascular endothelial growth factor family: identification of a fourth molec
A:Reference number: A41551; MUID:92168017
A:Accession: A41551

A:Molecule type: mRNA
A:Residues: 1-232 <H0U1>
A:Cross-references: GB:S85192; NID:g246155; PID:g246156
A:Accession: C41551
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-140, 'N', 183-232 <H0U2>
A:Accession: B41551
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-141, 227-232 <H0U>
R:Tischer, E.; Michell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.;
J. Biol. Chem. 266, 11947-11954, 1991
A:Title: The human gene for vascular endothelial growth factor. Multiple protein forms
A:Reference number: A40454; MUID:91268072
A:Accession: A40454
A:Molecule type: DNA
A:Residues: 1-165, 183-232 <T11>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976;
A:Accession: B40454
A:Molecule type: DNA
A:Residues: 1-140, 'N', 183-232 <T12>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63977;
A:Accession: C40454
A:Molecule type: DNA
A:Residues: 1-141, 227-232 <T13>
A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63978
R:Keck, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D.
Science 246, 1309-1312, 1989
A:Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.
A:Reference number: A40079; MUID:90069609
A:Accession: A40079
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-165, 183-232 <KEC>
A:Cross-references: GB:M27281; NID:g340300; PIDN:AAA36807.1; PID:g340301
R:Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.
Science 246, 1306-1309, 1989
A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.
A:Reference number: A40080; MUID:90069608
A:Accession: A40080
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140, 'N', 183-232 <LEU>
A:Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971
R>Weindel, K.; Marme, D.; Welch, H.A.
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992
A:Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endotheli
A:Reference number: JQ1463; MUID:92231879
A:Accession: JQ1463
A:Molecule type: mRNA
A:Residues: 1-140, 'N', 183-232 <WE1>
A:Cross-references: EMBL:X62568; NID:g37658; PIDN:CAA44447.1; PID:g37659
A:Experimental source: AIDS-Kaposi's sarcoma cell
A:Accession: JQ1464
A:Molecule type: mRNA
A:Residues: 1-140, 'N', 227-232 <WE2>
A:Experimental source: AIDS-Kaposi's sarcoma cell
R:Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.;
J. Biol. Chem. 264, 20017-20024, 1989
A:Title: Human vascular permeability factor. Isolation from U937 cells.
A:Reference number: A34492; MUID:90062112
A:Accession: A34492
A:Molecule type: protein
A:Residues: 27-36; 43-49, 'R'; 72-76, 'Q', 78-81; 59-71 <CON>
C:Comment: The most common of several alternatively spliced forms is VEGF 165.
C:Genetics:

A; Gene: GDB:VEGF
A; Cross-references: GDB:132244; OMIM:192240
A; Map position: 6p21-6p12
C; Function:
A; Description: promotes fluid and protein leakage from blood vessels
C; Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular

F;1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <V20
F;1-165,183-232/Product: vascular endothelial growth factor 189 precursor #status predicted
F;1-141,227-232/Product: vascular endothelial growth factor 121 precursor #status predicted
F;1-26/Domain: signal sequence #status predicted <SIG>
F;101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 104.5; DB 2; Length 232;
Best Local Similarity 27.0%; Pred. No. 0.0042;
Matches 24; Conservative 21; Mismatches 33; Indels 11; Gaps 4;

QY 25 CTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPVKYKHYEV 83
| | | | | : | | | | | : | | | | : | | | | : | | | | :
Db 52 CHPIETLVDIFQYDEYIEFKPCVPLMRCGG---CC--NDEGLECVPTESNITMQI 106
: | | | | : | | | | : | | | | : | | | | : | | | | :
QY 84 LQLPKTGVRLHLSLTDVALEHHEECDC 112
: | | | | : | | | | : | | | | : | | | | : | | | | :
Db 107 MRKPHQG-----QHIGEMSFLOHNKCEC 130
: | | | | : | | | | : | | | | : | | | | : | | | | :

RESULT 10
B28964
platelet-derived growth factor chain A precursor splice form 2 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: B28964; B42002; B28122
R;Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, and
A;Reference number: A28964; MUID: 88144463
A;Accession: B28964
A;Molecule type: DNA
A;Residues: 1-196 <BON>
A;Cross-references: GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M19986; GB:M19987; GB:
R;Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A;Title: Platelet-derived growth factor A chain: confirmation of localization of PDGFA t
A;Reference number: A42002; MUID: 92307656
A;Accession: B42002
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 152-196 <BO2>
R;Rorsman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betsholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988
A;Title: Structural characterization of the human platelet-derived growth factor A-chain
A;Reference number: A28122; MUID: 88174469
A;Accession: B28122
A;Molecule type: mRNA
A;Residues: 1-63, 'TRD', 67-196 <ROR>
A;Cross-references: GB:M20488
A;Note: the authors translated the codon ACA for residue 64 as Arg, C5T for residue 65 a
C;Comment: Exon 6 is spliced out of this variant splice form. For the major splice form
C;Genetics:
A;Gene: GDB:PDGFA
A;Cross-references: GDB:120266; OMIM:173430
A;Map position: 7p22-7p22
C;Superfamily: platelet-derived growth factor
C;Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet

Query Match 15.6%; Score 104; DB 2; Length 196;
Best Local Similarity 34.0%; Pred. No. 0.004;
Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;

QY 25 CTPRNFVSIR-REELKRTDTIF--WPGCLLVKRCGNCACCLHNCNEQCVPVKY---TK 78
| | | | | : | | | | | : | | | | | : | | | | : | | | | :
Db 96 CKTRVIVIEIPRSQVDPTSANFLIWPVCEVKRCGT---CC--NTSSVKQPSRVHRSV 150
: | | | | : | | | | : | | | | : | | | | : | | | | :
QY 79 KYHEVLQRLPKTGVRLHLSLTDVALEHHEECDC 112
| | | | | : | | | | | : | | | | | : | | | | : | | | | :
Db 151 KVAKVEYVRKPKLKEV-----QVRLEEHLECAC 179
: | | | | : | | | | : | | | | : | | | | : | | | | :

RESULT 11
S25096
platelet-derived growth factor chain A precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C;Accession: S25096; S33764
R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
submitted to the EMBL Data Library, July 1992
A;Description: Cross-species conservation in sequence and function of PDGF ligands and
A;Reference number: S25096
A;Accession: S25096
A;Molecule type: mRNA
A;Residues: 1-197 <HER1>
A;Cross-references: EMBL:Z14120; NID:g56865; PIDN:CAA78490.1; PID:g56866
R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
Biochim. Biophys. Acta 1173, 294-302, 1993
A;Title: Conservation in sequence and affinity of human and rodent PDGF ligands and r
A;Reference number: S33764; MUID: 93305723
A;Accession: S33764
A;Molecule type: mRNA
A;Residues: 89-172 <HER2>
A;Cross-references: EMBL:Z14120
C;Superfamily: platelet-derived growth factor
C;Keywords: growth factor; mitogen; platelet

Query Match 15.6%; Score 104; DB 2; Length 197;
Best Local Similarity 34.0%; Pred. No. 0.004;
Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;

QY 25 CTPRNFVSIR-REELKRTDTIF--WPGCLLVKRCGNCACCLHNCNEQCVPVKY---TK 78
| | | | | : | | | | | : | | | | | : | | | | : | | | | :
Db 89 CKTRVIVIEIPRSQVDPTSANFLIWPVCEVKRCGT---CC--NTSSVKQPSRVHRSV 143
: | | | | : | | | | : | | | | : | | | | : | | | | :
QY 79 KYHEVLQRLPKTGVRLHLSLTDVALEHHEECDC 112
| | | | | : | | | | | : | | | | | : | | | | : | | | | :
Db 144 KVAKVEYVRKPKLKEV-----QVRLEEHLECAC 172
: | | | | : | | | | : | | | | : | | | | : | | | | :

RESULT 12
PFHUG1
platelet-derived growth factor chain A precursor - human
N;Alternate names: PDGF A-chain; PDGF-1; PDGF-A; platelet-derived growth factor 1
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 18-Feb-2000
C;Accession: A28964; S47564; A42002; A01379; S00173; A28122
R;Bonthron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 1492-1496, 1988
A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal location
A;Reference number: A28964; MUID: 88144463
A;Accession: A28964
A;Molecule type: DNA
A;Residues: 1-211 <BON>
A;Cross-references: GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M19986; GB:M19987;
R;Takimoto, Y.; Kuramoto, A.
Biochim. Biophys. Acta 1222, 511-514, 1994
A;Title: Gene regulation by the 5'-untranslated region of the platelet-derived growth
A;Reference number: S47564; MUID: 94312450
A;Accession: S47564
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-21 <TAK>
R;Bonthron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.
Genomics 13, 257-263, 1992
A;Title: Platelet-derived growth factor A chain: confirmation of localization of PDGF
A;Reference number: A42002; MUID: 92307656
A;Accession: A42002
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 152-211 <BO2>
R;Betsholtz, C.; Johnsson, A.; Heidin, C.H.; Westermarck, B.; Lind, P.; Urdea, M.S.; E
Nature 320, 695-699, 1986
A;Title: cDNA sequence and chromosomal localization of human platelet-derived growth

A:Reference number: A01379; MUID:86203630
A:Accession: A01379
A:Molecule type: mRNA
A:Residues: 1-211 <BET>
A:Cross-references: GB:X03795; NID:g35365; PIDN:CAA27421.1; PID:g35366
A:Experimental source: clonal glioma cell line U-343 MGA12:6, a tumor cell line
R:Hoppe, J.; Schumacher, L.; Eichner, W.; Welch, H.A.
FEBS Lett. 223, 243-246, 1987
A:Title: The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only distantly
A:Reference number: S00173; MUID:88030061
A:Accession: S00173
A:Molecule type: mRNA
A:Residues: 1-193, 'DVR' <HOP>
A:Cross-references: EMBL:X06374; NID:g35363; PIDN:CAA29677.1; PID:g35364
R:Rossman, F.; Bywater, M.; Knott, T.J.; Scott, J.; Betscholtz, C.
Mol. Cell. Biol. 8, 571-577, 1988
A:Title: Structural characterization of the human platelet-derived growth factor A-chain
A:Reference number: A28122; MUID:88174698
A:Accession: A28122
A:Molecule type: mRNA
A:Residues: 1-63, 'TRD', 67-211 <ROR>
A:Cross-references: GB:M20488
A:Note: the authors translated the codon ACA for residue 64 as Arg, CGT for residue 65 as
C:Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal origin
C:Comment: A carboxyl-terminal propeptide may be removed from the precursor by proteolysis
C:Genetics:
A:Gene: GDB:PDGFA
A:Cross-references: GDB:120266; OMIM:173430
A:Map position: 7p22-7p22
A:Introns: 21/3; 54/1; 89/1; 151/3; 194/1
C:Complex: homodimer; heterodimer (see PIR:PFHUG2)
C:Superfamily: platelet-derived growth factor
C:Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet
E:1-20/Domain: signal sequence #status predicted <SIG>
E:21-86/Domain: propeptide #status predicted <PRO>
F:87-211/Product: platelet-derived growth factor chain A #status predicted <MAT>
F:158-162/Region: receptor binding #status predicted
F:96-140,129-177,133-179/Disulfide bonds: #status predicted
F:123/Disulfide bonds: interchain (to chain B-133 in heterodimeric form) #status predicted
F:123/Disulfide bonds: interchain (to 132 in homodimeric form) #status predicted
F:132/Disulfide bonds: interchain (to chain B-124 in heterodimeric form) #status predicted
F:132/Disulfide bonds: interchain (to 123 in homodimeric form) #status predicted
F:134/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.6%; Score 104; DB 1; Length 211;
Best Local Similarity 34.0%; Pred. No. 0.0043;
Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;
QY 25 CTPRNFVSII-REELKRTDTIF--WPGCLLVKRCGGNCACCLHNCNECCVPSKV---TK 78
DB 96 CKTRVIIVEIFRSQVDPTSANFLIWPVPCVEVRCGTG---CC--NTSSVRKQPSRVHRSV 150
QY 79 KYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDC 112
DB 151 KVAKVEYVRKPKLKEV-----QVRLEHLEAC 179
RESULT 13
TMVWSS
PDGF-related transforming protein (sis) - simian sarcoma virus
N:Alternate names: p28-sis
C:Species: simian sarcoma virus
C:Date: 23-Jul-1993 #sequence_revision 20-Sep-1984 #text_change 31-Oct-1997
C:Accession: A01381
R:Devare, S.G.; Reddy, E.P.; Law, J.D.; Robbins, K.C.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 80, 731-735, 1983
A:Title: Nucleotide sequence of the simian sarcoma virus genome: demonstration that its
A:Reference number: A03982; MUID:83144004
A:Accession: A01381
A:Molecule type: genomic RNA
A:Residues: 1-226 <DEV>
C:Genetics:

A:Gene: sis
C:Superfamily: platelet-derived growth factor
C:Keywords: growth factor; transforming protein
F:6-226/Domain: platelet-derived growth factor chain B similarity <PDG>
Query Match 15.6%; Score 104; DB 1; Length 226;
Best Local Similarity 33.3%; Pred. No. 0.0046;
Matches 36; Conservative 12; Mismatches 34; Indels 26; Gaps 9;
QY 16 LTEEVRVLSCTPRN--FSVSIREELKRTDTIF--WPGCLLVKRCGGNCACCLHNCNECCQ 71
DB 73 VAEPAMIAECKTRTEVEFIS--RRLIDRTNANFLVMPVPCVEVRCSG---CC--NNRNVCQ 126
QY 72 VPSVKTKYHEVLQRLP---KTGV---RGLHKSITDVALEHHEECDC 112
DB 127 RPTQV-----QLRPVQVRKIEIVRKPIFKKAT--VTLEDHLACK 165
RESULT 14
B49530
vascular endothelial growth factor homolog A2R, 14.7K - Orf virus
C:Species: Orf virus
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: B49530
R:Lytile, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o
A:Reference number: A49530; MUID:94076465
A:Contents: N22
A:Accession: B49530
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <LYT>
A:Cross-references: GB:S67520; NID:g456897; PIDN:AAB29220.1; PID:g456899
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:141420, NCBIPI:141425)
Query Match 15.4%; Score 102.5; DB 2; Length 133;
Best Local Similarity 30.5%; Pred. No. 0.004;
Matches 32; Conservative 18; Mismatches 40; Indels 15; Gaps 6;
QY 17 TEEVRLVLSCTPRNFSVSIRE---ELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECCQVP 73
DB 28 SEVLKSGECKPRPIVVPVSETHPEL--TSQRFNPPCVTLMRGCG---CC--NDSLECV 80
QY 74 SKVTYKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGST 118
DB 81 TEEVNVMTMELLG-ASGSGSNQMQR---LSFVHEKKCDRCRPFYT 120
RESULT 15
S52130
vascular endothelial growth factor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Accession: S52130
R:Sharma, H.S.; Tang, Z.H.; Gho, B.C.G.; Verdouw, P.D.
Biochim. Biophys. Acta 1260, 235-238, 1995
A:Title: Nucleotide sequence and expression of the porcine vascular endothelial growth
A:Reference number: S52130; MUID:95143284
A:Accession: S52130
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-190 <SHA>
A:Cross-references: GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560
Query Match 15.4%; Score 102.5; DB 2; Length 190;
Best Local Similarity 27.0%; Pred. No. 0.0055;
Matches 24; Conservative 20; Mismatches 34; Indels 11; Gaps 4;

Qy 25 CTPRNFVSIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNECOCVPSKYTKKYHEV 83
Db 51 CRPIETLVDIFQEYPDEIEYIFKPCVPLMRCGG---CC--NDEGLECVPTTEEFNITMQI 105
Qy 84 LOLRPKTGVRLHKLSTDVALEHHEECD 112
Db 106 MRKPHQG-----QHIGEMSFLOHNKCEC 129

Search completed: January 15, 2002, 22:17:35
Job time: 57 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2002, 22:20:38 ; Search time 24.01 Seconds
(without alignments)
183.248 Million cell updates/sec

Title: US-09-457-066-2_COPY_226_345

Perfect score: 666

Sequence: 1 AFVFGKSRVVDLNLTFEV.....DVALEHHECDVCVCGSTGG 120

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	114.5	17.2	148	1	VEGH_ORFN7
2	110	16.5	213	1	PDGA_RABIT
3	108.5	16.3	164	1	VEGF_CAVPO
4	108	16.2	241	1	PDGB_HUMAN
5	106	15.9	226	1	PDGA_XENLA
6	105.5	15.8	188	1	VEGB_HUMAN
7	105	15.8	245	1	PDGB_FELCA
8	104.5	15.7	215	1	VEGF_HUMAN
9	104	15.6	204	1	PDGA_RAT
10	104	15.6	211	1	PDGA_HUMAN
11	104	15.6	211	1	PDGA_MOUSE
12	104	15.6	226	1	TSIS_SMSAV
13	102.5	15.4	133	1	VEGH_ORFN2
14	102.5	15.4	190	1	VEGF_PIG
15	102.5	15.4	419	1	VEGC_HUMAN
16	101.5	15.2	146	1	VEGF_SHEEP
17	101.5	15.2	190	1	VEGF_BOVIN
18	101.5	15.2	415	1	VEGC_MOUSE
19	97	14.6	188	1	VEGB_MOUSE
20	96.5	14.5	190	1	VEGF_RAT
21	95.5	14.3	214	1	VEGF_MOUSE
22	94	14.1	225	1	PDGB_RAT
23	94	14.1	241	1	PDGB_MOUSE
24	88.5	13.3	216	1	VEGF_CHICK
25	88	13.2	241	1	PDGB_SHEEP
26	84	12.6	158	1	PLGF_MOUSE
27	83.5	12.5	5179	1	MUC2_HUMAN
28	79.5	11.9	170	1	PLGF_HUMAN
29	77.5	11.6	3672	1	LML2_CAEEL
30	73	11.0	60	1	MT_CHAAC
31	73	11.0	60	1	MT_PAGBE
32	73	11.0	60	1	MT_PACRC
33	72	10.8	60	1	MT_DICLA

```

RESULT 1
VEGH_ORFN7 171 10.8 72 10.8 171 1 LMB1_HYDAT
AC P52585; 3712 10.7 71.5 10.7 3712 1 LMA_DROME
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.
GN A2R.
OS Orf virus (strain NZ7) (OV NZ-7).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Parapoxvirus.
OX NCBI_TaxID=73495;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94076465; PubMed=8254780;
RA Lytle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;
RT "Homologs of vascular endothelial growth factor are encoded by the
RT poxvirus orf virus.";
RL J. Virol. 68:84-92(1994).
CC -1- FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; S67522; AAB29223.1; -
CC HSSP; P15692; LVPF.
CC InterPro; IPR000072; PDGF.
CC Pfam; PF00341; PDGF; 1.
CC ProDom; PD001629; PDGF; 1.
CC SMART; SM00141; PDGF; 1.
CC PROSITE; PS00249; PDGF_1; FALSE_NEG.
CC PROSITE; PS0278; PDGF_2; 1.
CC Mitogen; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 ?
FT CHAIN ? 148
FT VASCULAR ENDOTHELIAL GROWTH FACTOR
FT HOMOLOG
FT BY SIMILARITY.
FT DISULFID 46 88
FT DISULFID 77 130
FT DISULFID 81 132
FT INTERCHAIN (BY SIMILARITY).
FT DISULFID 71 71
FT INTERCHAIN (BY SIMILARITY).
FT DISULFID 80 80
FT CARBOHYD 95 95
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 148 AA; 16078 MW; F0E13BA104CC73F8 CRC64;

```

Query Match 17.2%; Score 114.5; DB 1; Length 148;
Best Local Similarity 30.2%; Pred No. 4.6e-05;
Matches : 29; Conservative 19; Mismatches 43; Indels 5; Gaps 3;

Matches 27; Conservative 21; Mismatches 37; Indels 17; Gaps 5;

Oy 18 EVRLYS-----CTPRNFSVIREL-KRTDTIFWPGCLLVKRCGNCACCLHNCQC 70
 ||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
 Db 12 EVKMDVYKRSYCRPIEMLVDFQEPDEIEYFKPSCVPLMRGCG---CC--NDESLE 66
 ||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
 Oy 71 CVPSKVTKKYHEVLORPKTGVRLGHLKSLTDVALEHHECDC 112
 ||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
 Db 67 CVPTTEFTMQRIMTKPHOG-----OHIGEMSFLOHSCKEC 103
 ||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :

RESULT 4
 PDGB_HUMAN
 ID PDGB_HUMAN STANDARD; PRT: 241 AA.
 AC P01127; P78431;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
 DE (PDGF-2) (C-SIS) (BECAPLERMIN).
 GN PDGFB OR SIS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84250225; PubMed=6740330;
 RA Josephs S.F., Ratner L., Clarke M.F., Westin E.H., Reitz M.S.,
 Wong-Staal F.;
 RT "Transforming potential of human c-sis nucleotide sequences encoding
 platelet-derived growth factor.";
 RL Science 225:636-639(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86205961; PubMed=3517869;
 RA Rao C.D., Igarashi H., Chiu I.-M., Robbins K.C., Aaronson S.A.;
 RT "Structure and sequence of the human c-sis/platelet-derived growth
 factor 2 (SIS/PDGF2) transcriptional unit.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2392-2396(1986).
 RN [3]
 RP SEQUENCE OF 22-241 FROM N.A.
 RX MEDLINE=84205633; PubMed=6327048;
 RA Chiu I.-M., Reddy E.P., Givol D., Robbins K.C., Tronick S.R.,
 Aaronson S.A.;
 RT "Nucleotide sequence analysis identifies the human c-sis
 proto-oncogene as a structural gene for platelet-derived growth
 factor.";
 RL Cell 37:123-129(1984).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85296313; PubMed=4033772;
 RA Collins T., Ginsburg D., Boss J.M., Orkin S.H., Pober J.S.;
 RT "Cultured human endothelial cells express platelet-derived growth
 factor B chain: cDNA cloning and structural analysis.";
 RL Nature 316:748-750(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85269623; PubMed=2991848;
 RA Ratner L., Josephs S.F., Jarrett R., Reitz M.S., Wong-Staal F.;
 RT "Nucleotide sequence of transforming human c-sis cDNA clones with
 homology to platelet-derived growth factor.";
 RL Nucleic Acids Res. 13:5007-5018(1985).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87217119; PubMed=3472769;
 RA Rao C.D., Igarashi H., Pech M.W., Robbins K.C., Aaronson S.A.;
 RT "Oncogenic potential of the human platelet-derived growth factor
 transcriptional unit.";
 RL Cold Spring Harb. Symp. Quant. Biol. 51:959-966(1986).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Burgess J., Odell C.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 1-53 FROM N.A.
 RX MEDLINE=97141927; PubMed=8981177;
 RA Simon M.-P., Pedoutour F., Sirvent N., Grosgeorge J., Minolletti F.,
 Coindre J.-M., Terrier-Lacombe M.-J., Wandahl N., Craver R.D.,
 Blin N., Sozzi G., Turc-Carel C., O'Brien K.P., Kedra D.,
 Fransson I., Guilbaud C., Dumanski J.P.;
 RT "Regulation of the platelet-derived growth factor B-chain gene via
 fusion with collagen gene COL1A1 in dermatofibrosarcoma protuberans
 and giant-cell-fibroblastoma.";
 RL Nat. Genet. 15:95-98(1997).
 RN [9]
 RP SEQUENCE OF 26-241 FROM N.A.
 RX MEDLINE=86164981; PubMed=345904;
 RA Weich H.A., Sebald W., Schairer H.U., Hoppe J.;
 RT "The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase
 mRNA which codes for the sequence of the PDGF-B chain.";
 RL FEBS Lett. 198:344-348(1986).
 RN [10]
 RP SEQUENCE OF 153-200 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=84236121; PubMed=6329745;
 RA Johnsson A., Heldin C.H., Wasteson A., Westermark B., Deuel T.F.,
 Huang J.S., Seeburg P.H., Gray A., Ullrich A., Scraze G.,
 Stroobant P., Waterfield M.D.;
 RT "The c-sis gene encodes a precursor of the B chain of
 platelet-derived growth factor.";
 RL EMBO J. 3:921-928(1984).
 RN [11]
 RP SEQUENCE OF 82-110.
 RX MEDLINE=83197379; PubMed=6844921;
 RA Antoniadis H.N., Hunkapiller M.W.;
 RT "Human platelet-derived growth factor (PDGF): amino-terminal amino
 acid sequence.";
 RL Science 220:963-965(1983).
 RN [12]
 RP SEQUENCE OF 82-112.
 RX MEDLINE=83244981; PubMed=6306471;
 RA Waterfield M.D., Scraze G.T., Whittle N., Stroobant P., Johnsson A.,
 Wasteson A., Westermark B., Heldin C.H., Huang J.S., Deuel T.F.;
 RT "Platelet-derived growth factor is structurally related to the
 putative transforming protein p28sis of simian sarcoma virus.";
 RL Nature 304:35-39(1983).
 RN [13]
 RP MUTAGENESIS, & IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR-BINDING.
 RX MEDLINE=92097530; PubMed=1661670;
 RA Clements J.M., Bawden L.J., Bloxidge R.E., Catlin G., Cook A.L.,
 Craig S., Drummond A.H., Edwards R.M., Fallon A., Green D.R.,
 Hellewell P.G., Kirwin P.M., Nayee P.D., Richardson S.J., Brown D.,
 Chahwala S.B., Snarey M., Winslow D.;
 RT "Two PDGF-B chain residues, arginine 27 and isoleucine 30, mediate
 receptor binding and activation.";
 RL EMBO J. 10:4113-4120(1991).
 RN [14]
 RP INTERCHAIN DISULFIDE BONDS.
 RX MEDLINE=92283833; PubMed=1317862;
 RA Andersson M., Oestman A., Baekstroem G., Hellman U.,
 George-Nascimento C., Westermark B., Heldin C.-H.;
 RT "Assignment of interchain disulfide bonds in platelet-derived growth
 factor (PDGF) and evidence for agonist activity of monomeric PDGF.";
 RL J. Biol. Chem. 267:11260-11266(1992).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=93010987; PubMed=1396586;
 RA Oefner C., D'Arcy A., Winkler F.K., Eggmann B., Hosang M.;
 RT "Crystal structure of human platelet-derived growth factor BB.";
 RL EMBO J. 11:3921-3926(1992).
 CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
 CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
 CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
 CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
 CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
 CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A

CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -!- PHARMACEUTICAL: AVAILABLE UNDER THE NAME REGRANEX (ORTHO-MCNEIL).
CC USED TO PROMOTE HEALING IN DIABETIC NEUROPATHIC FOOT ULCERS.
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -!- DATABASE: NAME=RAD Systems' cytokine source book;
CC WWW="http://www.rndsystems.com/cyt_cat/pdgm.html".
CC -!- DATABASE: NAME=Regranex; NOTE=Clinical Information on Regranex;
CC WWW="http://www.regranex.com/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01401; AAA60552.1; -
DR EMBL; K01918; AAA60552.1; JOINED.
DR EMBL; J00121; AAA60552.1; JOINED.
DR EMBL; K01398; AAA60552.1; JOINED.
DR EMBL; K01399; AAA60552.1; JOINED.
DR EMBL; K01400; AAA60552.1; JOINED.
DR EMBL; K02811; CAA26579.1; -
DR EMBL; M12783; AAA60553.1; -
DR EMBL; M02744; CAA26524.1; -
DR EMBL; K01817; AAA98793.1; -
DR EMBL; K01913; AAA98793.1; JOINED.
DR EMBL; K01914; AAA98793.1; JOINED.
DR EMBL; K01915; AAA98793.1; JOINED.
DR EMBL; K01916; AAA98793.1; JOINED.
DR EMBL; X03702; CAA27333.1; -
DR EMBL; Z81010; CAB02635.1; -
DR EMBL; X00561; CAA25228.1; -
DR EMBL; X00561; CAA25229.1; -
DR EMBL; X98706; CAA67262.1; -
DR PIR; A94276; PFHUG2.
DR PDB; 1PDG; 31-JAN-94.
DR MIM; 190040; -
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PDGF_1.
DR Pfam; PF00341; PDGF_1.
DR PRINTS; PR00438; GFCSKNOT.
DR PRODOM; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Mitogen; Growth factor; Proto-oncogene; Platelet; Signal;
KW Pharmaceutical; 3D-structure.
FT SIGNAL 1
FT PROPEP 21 80
FT CHAIN 82 190
FT PROPEP 191 241
FT SITE 108 108
FT SITE 111 111
FT DISULFID 97 141
FT DISULFID 130 178
FT DISULFID 134 180
FT DISULFID 124 124
FT DISULFID 133 133
FT CONFLICT 21 21
FT CONFLICT 101 101
FT CONFLICT 105 105
FT CONFLICT 107 107
Query Match 16.2%; Score 108; DB 1; Length 241;
Best Local Similarity 34.7%; Pred. NO. 0.00035;
Matches 42; Conservative 12; Mismatches 35; Indels 32; Gaps 11;
QY 5 GRKSRVVDNLTLT--EEVRLXSCTPRN--FSVSIRELKRTDTIF--WFGCLLVKRCGGN 58

Db 79 GRRS-----LGLSTTAEPAMIAECKTRTEVFEIS--RLIDRTNANFLVMPPCVEVQRCSG- 132
QY 59 CACCLHNCNOCQVPSKTKYHVLQLRP-----RTGV---RGLHKSITDVALEHHEED 111
Db 133 --CC--NNRNVCQRTQV-----QLRPQVVKIEIVRKPIFKKAT-VTLEDHLACK 179
QY 112 C 112
Db 180 C 180
RESULT 5
PDGA_XENLA
ID PDGA_XENLA STANDARD; PRT; 226 AA.
AC P13698;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
DE (PDGFA).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Oocyte;
RC MEDLINE=88321676; PubMed=3413486;
RA Mercola M., Melton D.A., Stiles C.D.;
RT "Platelet-derived growth factor A chain is maternally encoded in
RT Xenopus embryos";
RL Science 241:1223-1225(1988).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Oocyte;
RC MEDLINE=90175018; PubMed=2308861;
RA Bejcek B.E., Li D.Y., Deuel T.F.;
RT "Nucleotide sequence of a cDNA clone of Xenopus platelet-derived
RT growth factor A-chain";
RL Nucleic Acids Res. 18:680-680(1990).
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM
CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M23237; AAA49927.1; -
DR EMBL; M23238; AAA49928.1; -
DR EMBL; X17545; CAA35583.1; -
DR PIR; S08220; S08220.
DR HSSP; P01127; lPDG.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.

```

DR PRINTS: PR00438; GFCYSKNOT.
DR PRODM: PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL 1 22
FT PROPEP 23 91
FT CHAIN 92 226
FT DISULFID 101 145
FT DISULFID 134 182
FT DISULFID 138 184
FT DISULFID 128 128
FT DISULFID 137 137
FT CARBOHYD 139 139
FT VARSPLIC 198 200
FT VARSPLIC 201 226
FT CONFLICT 199 209
FT CONFLICT 218 218
SQ SEQUENCE 226 AA; 25719 MW; E3E724FCF67C2FB2 CRC64;

Query Match 15.9%; Score 106; DB 1; Length 226;
Best Local Similarity 30.6%; Pred. No. 0.00053;
Matches 38; Conservative 15; Mismatches 39; Indels 32; Gaps 9;

QY 6 RKSRRVVDLNLLEEVRLYSCYTPNFVSIVT-REELKRTDTIF--WPGCLLVKRCGNCACC 62
DB 88 RRRSV-----EEAVPAICKTQRTVIYIPRSQIDTPTSANFLIWPCCVEVKRCTG---CC 138
QY 63 LHCNECQCVPKSKYKHYH-----EVLQRLPKTGVRGLKSLTDVALEHHEECDCVC 114
DB 139 --NTSSVKQPSRI---HRSVKVAKVEVRKPK-----LKEVL--VRLEEHELECTTA 186
QY 115 RGST 118
DB 187 NSNS 190

RESULT 6
VEGB_HUMAN
ID VEGF_HUMAN STANDARD; PRT; 188 AA.
AC P49765;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR).
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96197355; PubMed=8637916;
RA Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V., Saksela O., Orpana A., Pettersson R.F., Alitalo K., Eriksson U.; "Vascular endothelial growth factor B, a novel growth factor for endothelial cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97077124; PubMed=8919691;
RA Grimmond S., Lagercrantz J., Drinkwater C., Silins G., Townson S., Pollock P., Gotley D., Carson E., Rakar S., Nordenskjold M., Ward L., Hayward N., Weber G.; "Cloning and characterization of a novel human gene related to vascular endothelial growth factor.";
RT Genome Res. 6:124-131(1996).
CC -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER

```

```

CC WITH VEGF.
CC -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.
CC HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
-----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
DR EMBL; U48801; AAB06274.1; -
DR EMBL; U43369; AAB91463.1; -
DR HSP; P15692; IVPF.
DR MIN; 601398; -
DR InterPro; IPR000072; PDGF.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.
KW Mitogen; Growth factor; Signal; Heparin-binding.
FT SIGNAL 1 21
FT CHAIN 22 188
FT SEQUENCE 188 AA; 21261 MW; F046345A3727194 CRC64;

Query Match 15.8%; Score 105.5; DB 1; Length 188;
Best Local Similarity 28.2%; Pred. No. 0.00049;
Matches 31; Conservative 22; Mismatches 40; Indels 17; Gaps 6;

QY 5 GRKSRVVD-LNLLTEEVRLYSCYTPNFVSIVT-REELKRT-DTIFWPGCLLVKRCGNCACC 62
DB 30 GHRKRVSWIDVYTRA----TCQPREVVVPLTVELMGTVAKQLVPCVTVQRCGG---CC 82
QY 63 LHCNECQCVPKSKYKHYHVEVLQRLPKTGVRGLKSLTDVALEHHEECDC 112
DB 83 PD--DGLQCVPTGQHVQRMQILIRYPS-----SQLGEMSLSEHSQCEC 124

RESULT 7
PDGB_FELCA
ID PDGB_FELCA STANDARD; PRT; 245 AA.
AC P12919;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN) (PDGF) (C-SIS) (PDGF-2).
DE (PDGF) OR SIS.
GN PDGFB OR SIS.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87146463; PubMed=3822831;
RA van den Ouweland A.M.W., van Groningen J.J.M., Schalken J.A., van Neck H.W., Bloemers H.P.J., van de Ven W.J.M.; "Genetic organization of the c-sis transcription unit.";
RT Nucleic Acids Res. 15:959-970(1987).
RN [2]
RP REVISIONS.
RA van den Ouweland A.M.W.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE

```

```

CC CC      IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC CC      -! SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC CC      AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC CC      TRANSFORMATION PROCESSES.
CC CC      -! MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC CC      PDGF RECEPTOR.
CC CC      -! SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC      the European Bioinformatics Institute. There are no restrictions on its
CC CC      use by non-profit institutions as long as its content is in no way
CC CC      modified and this statement is not removed. Usage by and for commercial
CC CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
CC CC      EMBL: X05112; CAA28758.1; ALT_SEQ.
CC CC      PIR: A26402; TVCTSS.
CC CC      HSSP: P01127; LPDG.
CC CC      InterPro: IPR002400; GF_cysknot.
CC CC      InterPro: IPR000072; PDGF.
CC CC      Pfam: PF00341; PDGF; 1.
CC CC      PRINTS: PR00438; GFCYSKNOT.
CC CC      ProDom: PD001629; PDGF; 1.
CC CC      SMART: SM00141; PDGF; 1.
CC CC      PROSITE: PS00249; PDGF_1; 1.
CC CC      PROSITE: PS00278; PDGF_2; 1.
CC CC      Mitogen: Growth factor; Proto-oncogene; Platelet; Signal.
CC CC      SIGNAL 1 20 BY SIMILARITY.
CC CC      FT PROPEP 21 81
CC CC      FT CHAIN 82 194 PLATELET-DERIVED GROWTH FACTOR, B CHAIN.
CC CC      FT PROPEP 195 245
CC CC      FT DISULFID 101 145 BY SIMILARITY.
CC CC      FT DISULFID 134 182 BY SIMILARITY.
CC CC      FT DISULFID 138 184 BY SIMILARITY.
CC CC      FT DISULFID 128 138 INTERCHAIN (BY SIMILARITY).
CC CC      FT DISULFID 137 137 INTERCHAIN (BY SIMILARITY).
CC CC      SQ SEQUENCE 245 AA; 27787 MW; E715291D9837512 CRC64;

Query Match 15.8%; Score 105; DB 1; Length 245;
Best Local Similarity 33.0%; Pred. No. 0.00072;
Matches 35; Conservative 13; Mismatches 36; Indels 22; Gaps 8;

QY 16 LIEEVRLYSGTTPRN--FSVSIRELKRDTIF--WPGCLLVKRGCGNACGLHNCNEQC 71
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
92 VAEPAMIAECKTRTEFEVS--RLIDRTNANFLWPPCEVQRCSG---CC--NNRNVCQ 145
QY 72 VPSKVTKKY-----HEVLQLRPKTVGRGLHKLSTDALEHHEECDC 112
Db : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
146 RPTQVOLRLVQVRKIEIVRRP-----VFKKAT-VTLEDHLACKC 184

RESULT 8
VEGF_HUMAN
ID VEGF_HUMAN STANDARD; PRT; 215 AA.
AC P15692;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGFG) (VASCULAR
DE PERMEABILITY FACTOR) (VPF).
GN VEGF OR VEGFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90069608; PubMed=2479986;
RA Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;
RT "Vascular endothelial growth factor is a secreted angiogenic
mitogen.";

```

```

RL Science 246:1306-1309(1989).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=90069609; PubMed=2479987;
RA Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J.,
RA Connolly D.T.;
RT "Vascular permeability factor, an endothelial cell mitogen related to
RT PDGF.";
RL Science 246:1309-1312(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91268072; PubMed=1711045;
RA Fischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D.,
RA Fiddes J.C., Abraham J.A.;
RT "The human gene for vascular endothelial growth factor. Multiple
RT protein forms are encoded through alternative exon splicing.";
RL J. Biol. Chem. 266:11947-11954(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92231879; PubMed=1567395;
RA Weindel K., Marne D., Weich H.A.;
RT "AIDS-associated Kaposi's sarcoma cells in culture express vascular
RT endothelial growth factor.";
RL Biochem. Biophys. Res. Commun. 183:1167-1174(1992).
RN [5]
RP PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.
RX MEDLINE=90062112; PubMed=2584205;
RA Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,
RA Siegel N., Haymore B.L., Leimgruber R., Feder J.;
RT "Human vascular permeability factor. Isolation from U937 cells.";
RL J. Biol. Chem. 264:20017-20024(1989).
RN [6]
RP SEQUENCE OF 27-41.
RX MEDLINE=93145946; PubMed=7678805;
RA Fiebig B.L., Jaeger B., Schoellmann C., Weindel K., Wiltling J.,
RA Kochs G., Marne D., Hug H., Weich H.A.;
RT "Synthesis and assembly of functionally active human vascular
RT endothelial growth factor homodimers in insect cells.";
RL Eur. J. Biochem. 211:19-26(1993).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.
RX MEDLINE=97352774; PubMed=9207067;
RA Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,
RA de Vos A.M.;
RT "Vascular endothelial growth factor: crystal structure and functional
RT mapping of the kinase domain receptor binding site.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.
RX MEDLINE=98035455; PubMed=9351807;
RA Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;
RT "The crystal structure of vascular endothelial growth factor (VEGFG)
RT refined to 1.93-A resolution: multiple copy flexibility and receptor
RT binding.";
RL Structure 5:1325-1338(1997).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.
RX MEDLINE=99119204; PubMed=9922142;
RA Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,
RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;
RT "Crystal structure of the complex between VEGF and a receptor-blocking
RT peptide.";
RL Biochemistry 37:17765-17772(1998).
RN [10]
RP STRUCTURE BY NMR OF 34-135.
RX MEDLINE=97477915; PubMed=9336848;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RA Starovasnik M.A.;
RT "1H, 13C, and 15N backbone assignment and secondary structure of the
RT receptor-binding domain of vascular endothelial growth factor.";
RL Protein Sci. 6:2250-2260(1997).
RN [11]
RP STRUCTURE BY NMR OF 137-215.

```

RX MEDLINE=98298440; PubMed=9634701;
RA Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,
RT "Solution structure of the heparin-binding domain of vascular
RL endothelial growth factor.";
CC Structure 6:637-648(1998).
CC -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC PERMEABILITY.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: FOUR FORMS OF VEGF ARE PRODUCED BY
CC ALTERNATIVE SPLICING OF THE SAME GENE (VEGF-121, VEGF-165,
CC VEGF-189 AND VEGF-215).
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M32977; AAA35789.1; -
DR EMBL; M27281; AAA36807.1; -
DR EMBL; M63978; AAA36804.1; -
DR EMBL; M63971; AAA36804.1; JOINED.
DR EMBL; M63972; AAA36804.1; JOINED.
DR EMBL; M63973; AAA36804.1; JOINED.
DR EMBL; M63974; AAA36804.1; JOINED.
DR EMBL; M63975; AAA36804.1; JOINED.
DR EMBL; M63976; AAA36804.1; JOINED.
DR EMBL; M63977; AAA36804.1; JOINED.
DR EMBL; M62568; CAA44447.1; -
DR PIR; A34492; A34492.
DR PIR; A40079; A40079.
DR PIR; A40080; A40080.
DR PIR; A40454; A40454.
DR PIR; B40454; B40454.
DR PIR; C40454; C40454.
DR PIR; JQ1463; JQ1463.
DR PIR; JQ1464; JQ1464.
DR PIR; S17348; S17348.
DR PDB; 1VGH; 08-APR-98.
DR PDB; 2VGH; 08-APR-98.
DR PDB; 1VFF; 08-APR-98.
DR PDB; 2VFF; 29-JUL-98.
DR PDB; 1VPP; 23-FEB-99.
DR MIM; 192240; -
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS00278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Alternative splicing; Signal;
KW 3D-structure.
FT SIGNAL 1 26
FT CHAIN 27 215
FT DISULFID 52 94
FT DISULFID 83 128
FT DISULFID 87 130
FT DISULFID 77 77
FT DISULFID 86 86
FT CARBOHYD 101 101
FT VARSPPLIC 141 141
FT VARSPLIC 142 165
FT VARSPLIC 142 209
FT SEQUENCE 215 AA; 25173 MW; 7B9759AD5871FF33 CRC64;
SQ

Query Match 15.7%; Score 104.5; DB 1; Length 215;
Best Local Similarity 27.0%; Pred. No. 0.00071;
Matches 24; Conservative 21; Mismatches 33; Indels 11; Gaps 4;
Qy 25 CTPNFSVISREEL-KRTDTTFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKYHEV 83
| | | | | : | | | | | : | | | | | : | | | | | :
Db 52 CHPIETLVDFIQEYDFEYIFKPSCVPLMRGCG---CC--NDEGLECVPTESNITMOI 106
| | | | | : | | | | | : | | | | | : | | | | | :
Qy 84 LQLRPKTVGRGLHKLSDVALEHHEECDC 112
| | | | | : | | | | | : | | | | | : | | | | | :
Db 107 MRIRPHQG-----OHIGEMSFLOHNRKCEC 130
| | | | | : | | | | | : | | | | | : | | | | | :
RESULT 9
PDGA_RAT
ID PDGA_RAT STANDARD; PRT; 204 AA.
AC P28576;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
DE (PDGF-1).
GN PDGFA OR RPAL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 8-204 FROM N.A.
RX MEDLINE=93305723; PubMed=8318539;
RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;
RT "Conservation in sequence and affinity of human and rodent PDGF
RT ligands and receptors.";
RL Biochim. Biophys. Acta 1173:294-302(1993).
[2]
RX SEQUENCE FROM N.A.
RX MEDLINE=93191115; PubMed=8447423;
RA Katayose D., Ohe M., Yamauchi K., Ogata M., Shirato K., Fujita H.,
RT Shibahara S., Takishima T.;
RT "Increased expression of PDGF A- and B-chain genes in rat lungs with
RT hypoxic pulmonary hypertension.";
RL Am. J. Physiol. 264:L100-L106(1993).
[3]
RX SEQUENCE FROM N.A. (SHORT FORM).
RA Xia Y., Feng L., Tang W.W., Wilson C.B.;
RT "Cloning and expression of rat platelet-derived growth factor
RT A-chain.";
RL J. Am. Soc. Nephrol. 3:622-622(1992).
[4]
RX SEQUENCE OF 58-196 FROM N.A. (SHORT FORM).
RX STRAINE-FISCHER 344; TISSUE-Smooth muscle;
RX MEDLINE=93225589; PubMed=8469035;
RA Szabo P., Weksler D., Whittington E., Weksler B.B.;
RT "The age-dependent proliferation of rat aortic smooth muscle cells is
RT independent of differential splicing of PDGF A-chain mRNA.";
RL Mech. Ageing Dev. 67:79-89(1993).
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM
CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.
CC -!- DEVELOPMENTAL STAGE: IN KIDNEY EPITHELIAL TISSUES, THE SHORTER
CC FORM PREDOMINATES IN YOUNG (1 DAY OLD) RATS WHILE THE LONGER FORM
CC BECOMES MORE PREVALENT DURING AGING.
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE

FT	DISULFID	82	127	BY SIMILARITY.
FT	DISULFID	86	129	BY SIMILARITY.
FT	DISULFID	76	76	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	85	85	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	100	100	N-LINKED (GLCNAC...) (POTENTIAL).
SEQ	SEQUENCE	190 AA;	22368 MW;	04D40B8D7913047F CRC64;

Query Match 15.4%; Score 102.5; DB 1; Length 190;
Best Local Similarity 27.0%; Pred. No. 0.001;
Matches 24; Conservative 20; Mismatches 34; Indels 11; Gaps 4;

QY	25	CTPRNFSVSTREEL-KRTDTRFWPGLLVKRCGNCACCLHNCNOCVCSKVTKYKHEV	83
Db	51	CRPIETLWDFQEPDEITEVIFKPSVPLMRGCG--CC--NDRGLECVPTPEFNITMQI	105
		: : : : : : : : : : : : : : : : : : :	
QY	84	LQLRPKTVGRGLHSLTDVALEHHECDC	112
Db	106	MRIRPHOG-----OHIGEMSFLOHNKCEC	129

RESULT 15
VEGC_HUMAN STANDARD; PRT; 419 AA.

ID	VEGC_HUMAN	STANDARD;	PRT;	419 AA.
AC	P49767;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR			
DE	ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4-			
DE	L).			
GN	VEGFC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.			
RX	MEDLINE=96178224; PubMed=8617204;			
RA	Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,			
RA	Saksela O., Kalkkinen N., Alitalo K.;			
RT	"A novel vascular endothelial growth factor, VEGF-C, is a ligand for			
RT	the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";			
RL	EMBO J. 15:290-298(1996).			
RN	[2]			
RP	ERRATUM.			
RX	MEDLINE=96203094; PubMed=8612600;			
RA	Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,			
RA	Saksela O., Kalkkinen N., Alitalo K.;			
RL	EMBO J. 15:1751-1751(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96312526; PubMed=8700872;			
RA	Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;			
RT	"Vascular endothelial growth factor-related protein: a ligand and			
RT	specific activator of the tyrosine kinase receptor Flt4.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R.,			
RA	Burgess P., Giannotti J., Charletta A., Hennessey D., Kovacic S.,			
RA	Fitzgerald M., Scaltreto H., Welch N., Neben S., Finnerty H.,			
RA	Zoller R., Wang J., Nickbarg E., Gassaway R., Turner K.,			
RA	Wood C.R.;			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL			
CC	CELL GROWTH.			
CC	-1- SUBUNIT: HOMODIMER: DISULFIDE-LINKED.			
CC	-1- PTM: PROBABLY PROTEOLITICALLY PROCESSED IN THE C-TERMINUS.			
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	-----			

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL; X94216; CAA53907.1; -;	InterPro: IPR002400; GF_cysknot.
EMBL; U43142; AAB85214.1; -;	InterPro: IPR000072; PDGF.
EMBL; U58111; AAB02909.1; -;	Pfam: PF00341; PDGF; 1.
HSP; P15692; 1VPF.	PRINTS; PR00438; GFCYSKNOT.
MIM; 601528; -;	ProDom; PD001629; PDGF; 1.
	SMART; SM00141; PDGF; 1.
	PROSITE; PS00249; PDGF_1; 1.
	PROSITE; PS0278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat.	
FT SIGNAL 1 ?	POTENTIAL.
FT PROPEP ?	POTENTIAL.
FT CHAIN 103 419	VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT DOMAIN 275 365	4 X 24 AA TANDEM REPEATS.
FT REPEAT 275 298	1.
FT REPEAT 299 322	2.
FT REPEAT 323 346	3.
FT REPEAT 347 365	4 (PARTIAL).
FT CARBOHYD 175 175	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 419 AA; 46883 MW; 9F598719DB3E014F CRC64;	
SQL	

Search completed: January 15, 2002, 22:22:37
Job time: 119 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2002, 22:17:38 ; Search time 58.55 Seconds
(without alignments)
299.790 Million cell updates/sec

Title: US-09-457-066-2_COPY_226_345
Perfect score: 666
Sequence: 1 AFVFGKSRVVDLNLLEEV.....DVALEHHEDCVCVRGSGG 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	666	100.0	345	4 Q9UL22	Q9UL22 homo sapien
2	666	100.0	345	4 Q9NRA1	Q9NRA1 homo sapien
3	624	93.7	345	11 Q9QY71	Q9QY71 mus musculus
4	611	91.7	345	11 Q9EQX6	Q9EQX6 rattus norv
5	608	91.3	345	11 Q9JHV8	Q9JHV8 mus musculus
6	585	87.8	345	13 Q9I946	Q9I946 gallus gall
7	324	48.6	290	11 Q9DIL8	Q9DIL8 mus musculus
8	324	48.6	364	4 Q9BRV5	Q9BRV5 homo sapien
9	324	48.6	370	4 Q9GZP0	Q9GZP0 homo sapien
10	324	48.6	370	11 Q9EQT1	Q9EQT1 rattus norv
11	180	27.0	34	11 Q99JM4	Q99JM4 mus musculus
12	121.5	18.2	326	11 Q35251	Q35251 rattus norv
13	119.5	17.9	358	11 P97946	P97946 mus musculus
14	115.5	17.3	354	4 O43915	O43915 homo sapien
15	108.5	16.3	148	13 O42571	O42571 xenopus lae
16	108.5	16.3	194	13 O42572	O42572 xenopus lae
17	108	16.2	185	4 Q15354	Q15354 homo sapien
18	108	16.2	226	4 Q9UF23	Q9UF23 homo sapien
19	105.5	15.8	207	4 Q16528	Q16528 homo sapien

20	105	15.8	210	6 Q29613	Q29613 felis silve
21	104.5	15.7	126	6 Q9BDP7	Q9BDP7 macaca mula
22	104.5	15.7	147	4 Q9UH58	Q9UH58 homo sapien
23	104.5	15.7	171	4 Q9H1W8	Q9H1W8 homo sapien
24	104.5	15.7	174	4 Q9UL23	Q9UL23 homo sapien
25	104.5	15.7	209	4 Q60720	Q60720 homo sapien
26	104.5	15.7	232	4 Q9H1W9	Q9H1W9 homo sapien
27	104.5	15.7	254	4 Q16889	Q16889 homo sapien
28	104	15.6	118	11 Q9CU96	Q9CU96 mus musculus
29	104	15.6	196	11 Q9UL56	Q9UL56 mus musculus
30	102.5	15.4	190	6 Q9XSF3	Q9XSF3 canis famil
31	102.5	15.4	190	6 Q9GLS2	Q9GLS2 sus scrofa
32	102.5	15.4	208	6 Q9XSF4	Q9XSF4 canis famil
33	102.5	15.4	214	6 Q9XSF5	Q9XSF5 canis famil
34	102.5	15.4	214	6 Q9MYV3	Q9MYV3 canis famil
35	102	15.3	188	6 Q9XS48	Q9XS48 bos taurus
36	102	15.3	193	6 Q9XS49	Q9XS49 bos taurus
37	102	15.3	301	5 Q9VWP6	Q9VWP6 drosophila
38	102	15.3	314	5 Q9BLX1	Q9BLX1 drosophila
39	101.5	15.2	118	6 Q9MZB1	Q9MZB1 ovis aries
40	101.5	15.2	124	6 Q9GK00	Q9GK00 callithrix
41	101.5	15.2	190	6 Q77643	Q77643 ovis aries
42	101.5	15.2	418	13 Q57352	Q57352 coturnix co
43	101.5	15.2	420	6 Q9XS50	Q9XS50 bos taurus
44	100.5	15.1	144	13 Q73822	Q73822 brachydanio
45	100.5	15.1	188	13 Q73682	Q73682 brachydanio

ALIGNMENTS

RESULT 1
Q9UL22
ID Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED GROWTH FACTOR).
DE HSCDGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Tsai Y.J., Lee R.K.K., Lin S.P.;
RT "Pallotein, a novel growth factor like gene identified in human uterus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Uti-Tel K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique member of the PDGF/VEGF family.";
FEBS Lett. 475:97-102(2000).
DR EMBL; AF091434; AA000049.1; -;
DR EMBL; AB033831; BAB03286.1; -;
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000702; PDGF.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF.2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 100.0%; Score 666; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.7e-68;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
|||||
Db 226 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 285
|||||

Qy 61 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 120
|||||
Db 286 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 345
|||||

RESULT 2
Q9NR1 PRELIMINARY; PRT; 345 AA.

AC Q9NR1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Betsholtz C., Heldin C.-H., Alltalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a novel protease-activated ligand for the PDGF alpha
RT receptor";
RL Nat. Cell Biol. 0:0-0(2000).
DR EMBL: AF244813; AAF80597.1; -;
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00341; PDGF; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 100.0%; Score 666; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.7e-68;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
|||||
Db 226 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 285
|||||

Qy 61 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 120
|||||
Db 286 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 345
|||||

RESULT 3
Q9QY71 PRELIMINARY; PRT; 345 AA.

AC Q9QY71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE FALLOTIN.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RT "cDNA cloning of falloletin from mouse ovary";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF117608; AAF22516.1; -;
DR MGB: MGI:1859631; Pdgcfc.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

Query Match 93.7%; Score 624; DB 11; Length 345;
Best Local Similarity 90.8%; Pred. No. 3.5e-63;
Matches 109; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
|||||
Db 226 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 285
|||||

Qy 61 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 120
|||||
Db 286 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGNAGG 345
|||||

RESULT 4
Q9EQX6 PRELIMINARY; PRT; 345 AA.

ID Q9EQX6;
AC Q9EQX6;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SPINAL CORD-DERIVED GROWTH FACTOR.
GN RSCDGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=KIDNEY;
RA Hanada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
RL SCDF/PDGF-C/falloletin";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
DR EMBL: AB033830; BAB19969.1; -;
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 91.7%; Score 611; DB 11; Length 345;
Best Local Similarity 89.2%; Pred. No. 1.1e-61;
Matches 107; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 60
|||||
Db 226 AFVFGKSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCA 285
|||||

Qy 61 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG 120
|||||
Db 286 CCLHNCNECQVPSKVTKYHEVLQRLPKTGVRLGHLKSLTDVALEHHEECDCVCRGNTEG 345
|||||

[illegible]

RESULT 9

Q9GZPO	PRELIMINARY;	PRT;	370 AA.
ID	Q9GZPO		
AC	Q9GZPO;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	SPINAL CORD-DERIVED GROWTH FACTOR-B (MSTP036) (IRIS-EXPRESSED GROWTH		
DE	FACTOR LONG FORM).		
GN	HSCDGF-B OR IEGF.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Hamada T., Ui-Tei K., Imaki J., Miyata Y.;		
RT	"Molecular Cloning of SCDFG-B, a Novel Growth Factor Homologous to		
RT	SCDFG/PDGF-C/fallotainin."		
RL	Biochem. Biophys. Res. Commun. 0:0-0(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	LIU B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,		
RA	Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,		
RA	Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.		
RA	Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;		
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.		

		Query Match	48.6%	Score 324;	DB 11;	Length 370;
		Best Local Similarity	52.7%;	Pred. No. 6.6e-29;		
		Matches	59;	Conservative	18;	Mismatches 31; Indels 4; Gaps 2;
Qy	6	RKSRVDLNLITTEVRVLYSCTPRNFSYSIREELKTDTFIWPGCLLVYRCGGNCACCLHN	65			
		: : : : : : : : : : : :				
Dd	254	RKSK-VDLDRUNDVKRYSCIPRNHNVNREELKLTNAVFPRCLLVQRCCGNGCGTLN	312			
		: : : : : : : : : : : : : :				
Qy	66	CNEQCQVPKSVTKKYHEVLQLRP---KTGVRLGHKSILTDVALEHHEEDCVCV	114			
		: : : : : : : : : : : : : :				

RESULT 14
O43915 PRELIMINARY; PRT; 354 AA.
AC O43915;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GROWTH FACTOR FIGF.
GN FIGF OR VEGF-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RX MEDLINE=98140120; PubMed=9479493;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT between the FIGA and the GRPR genes.";
RL Genomics 47:207-216(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada Y., Nezu J., Shimane M., Hirata Y.;
RL "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
RA Allitalo K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
DR EMBL; Y12864; CAA73371.1; JOINED.
DR EMBL; Y12865; CAA73371.1; JOINED.
DR EMBL; Y12866; CAA73371.1; JOINED.
DR EMBL; Y12867; CAA73371.1; JOINED.
DR EMBL; Y12868; CAA73371.1; JOINED.
DR EMBL; Y12869; CAA73371.1; JOINED.
DR EMBL; Y12870; CAA73371.1; JOINED.
DR EMBL; D89830; BAA24264.1; JOINED.
DR EMBL; AJ000185; CAA03942.1; JOINED.
DR EMBL; Y12863; CAA73370.1; JOINED.
DR HSSP; P15692; 1VPP.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF; 1.
DR PROSITE; PS02078; PDGF; 2.
SQ SEQUENCE 354 AA; 40444 MW; 2048D769D735173E CRC64;

Query Match 17.3%; Score 115.5; DB 4; Length 354;
Best Local Similarity 33.0%; Pred. No. 3.9e-05;
Matches 34; Conservative 14; Mismatches 44; Indels 11; Gaps 5;

Qy 13 LNLTEVRLKSYCTPRNFSVIREEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNEC-Q 70
| : : : : : | : : : : : | : : : : : | : : : : : |
Dy 99 LKVIDEEQRTQCSPRETCVEVASELGKSTNTFFKPCVNVFRCGG---CCNEESLICMN 155
| : : : : : | : : : : : | : : : : : | : : : : : |

Qy 71 CVPSKVTKKYHEVLQLRPKTVGRLHKSITDVALEHHEECDCV 113
| : : : : : | : : : : : | : : : : : | : : : : : |
Dy 156 TSTVTSIKQLFEISV--PLTSV-----PELVPRKVNHTGCKCL 192

RESULT 15
O42571 PRELIMINARY; PRT; 148 AA.
AC O42571;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR 122.
GN VEGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RX MEDLINE=98140120; PubMed=9479493;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
RT between the FIGA and the GRPR genes.";
RL Genomics 47:207-216(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada Y., Nezu J., Shimane M., Hirata Y.;
RL "Molecular cloning of a novel vascular endothelial growth factor,
RT VEGF-D.";
RL Genomics 42:483-488(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitali A., Wilks A.F.,
RA Allitalo K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
RT tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
DR EMBL; Y12864; CAA73371.1; JOINED.
DR EMBL; Y12865; CAA73371.1; JOINED.
DR EMBL; Y12866; CAA73371.1; JOINED.
DR EMBL; Y12867; CAA73371.1; JOINED.
DR EMBL; Y12868; CAA73371.1; JOINED.
DR EMBL; Y12869; CAA73371.1; JOINED.
DR EMBL; Y12870; CAA73371.1; JOINED.
DR EMBL; D89830; BAA24264.1; JOINED.
DR EMBL; AJ000185; CAA03942.1; JOINED.
DR EMBL; Y12863; CAA73370.1; JOINED.
DR HSSP; P15692; 1VPP.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF; 1.
DR PROSITE; PS02078; PDGF; 2.
SQ SEQUENCE 354 AA; 40444 MW; 2048D769D735173E CRC64;

Query Match 16.3%; Score 108.5; DB 13; Length 148;
Best Local Similarity 25.8%; Pred. No. 0.0001;
Matches 23; Conservative 21; Mismatches 34; Indels 11; Gaps 4;

Qy 25 CTPRNFSVSIREEEL-KRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEV 83
| : : : : : | : : : : : | : : : : : | : : : : : |
Dy 52 CQVREILVDIFQEYDPDEVEYIFKPSCVPLMRCAG---CC--NDESLECVPTCYNITMQI 106
| : : : : : | : : : : : | : : : : : | : : : : : |

Qy 84 LQLRPKTGVRGLHKSITDVALEHHEECDC 112
| : : : : : | : : : : : | : : : : : | : : : : : |
Dy 107 MKIRPH-----ISQHIMDSFQHSQCEC 130

Search completed: January 15, 2002, 22:21:53
Job time: 255 sec
```

OM of: US-09-457-066-2_COPY_226_345 to: EST:* out_format : pfs

Date: Jan 15, 2002 10:42 PM

About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

```

MODEL=framecat_p2n.model -DEV=xlh
-Q/CGN2_1/UFMT-spool/US09457086/runat_15012002_132155_14189/app_query.fasta_1.190
-DB=est -JPMO-fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPLC=0.000 -LOOPEXT=0.000 -GGAPOP=4.500
-QCAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human4.0.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pts -NORM=ext -HEAPSIZ=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09457066.@CGN1.1.3596
-NGPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

```

Search information block:

Query: US-09-457-066-2 COPY 226 345

Query length: 120

Database: EST: *

Database sequences: 11351937

Database length: 1077921985

```
Search time (sec): 1201.300000
```

score_list:

Sequence	Strd	Orig	Zscore	EScore	Len	Documentation
gb_est2:BG681390	+	660.00	1229.82	2.4e-59	1142	! BG681390 602627750F1 NCI_CGAP_1
gb_est2:BG185961	+	652.00	1218.10	1.1e-58	811	! BG185961 RS74916 Athersys RAGE
gb_est2:BF021679	+	624.00	1169.60	5.5e-56	523	! BF021679 y05f005.y1 NCI_CGAP_1
gb_est2:BF958470	+	620.00	1162.06	1.5e-55	523	! BE958470 601644787F1 NIH_MGC_56
gb_est2:BG609411	+	620.00	1161.46	1.6e-55	556	! BG609411 323251 MARC 1P1G Sus
gb_est2:BG677432	+	617.00	1160.73	6.3e-55	969	! BG677432 602625259F1 NCI_CGAP_5
gb_est2:BF151335	+	590.00	1150.43	2.3e-52	564	! BF151335 uz15b12.y1 NCI_CGAP_Ma
gb_est1:AA047637	+	568.00	1069.31	2.1e-50	304	! AA047637 DKFZp586J0421.r1 586
gb_est2:BG243001	+	566.00	1054.76	1.4e-49	910	! BG243001 602355974F1 NCI_CGAP_M
gb_est2:BF102859	+	552.50	1029.95	3.3e-48	851	! BF102859 601646827F1 NIH_MGC_58
gb_est2:BF031624	+	523.00	973.23	4.8e-45	950	! BF031624 601558104F1 NIH_MGC_58
gb_est2:BF011835	+	514.00	963.67	1.6e-44	447	! BF011835 us37d10.y1 Soares_NHEK
gb_est2:BF617092	+	463.00	860.88	8.7e-39	874	! BF617092 602119417F1 NIH_MGC_50
gb_est2:BF617092	+	442.00	820.27	1.6e-36	968	! BG118707 60233492801F1 NIH_MGC_50
gb_gss:CN5024MX	-	397.00	736.36	7.5e-32	877	! AL180978 Tetraodon nigroviridis
gb_est2:BF163629	+	381.00	705.91	3.7e-30	902	! BF163629 601769732F1 NCI_CGAP_1
gb_est2:BG692935	+	339.00	632.14	4.8e-26	518	! BG692935 342806 BARC 5Bov Bos t
gb_hlc:AK003359	+	324.00	591.62	8.6e-24	1796	! AK003359 Mus musculus 18 days
gb_est1:BE374398	+	323.50	602.85	2.0e-24	521	! BE374398 601227568F1 NCI_CGAP_M
gb_est1:AA702581	+	294.00	476.44	2.3e-17	324	! AA702581 ua36f08.r1 Soares_mamm
gb_est1:AA759138	+	254.00	473.77	3.2e-17	425	! AA759138 ah78c03.s1 Soares_test
gb_gss:CN50458A	-	217.50	396.16	6.7e-13	1036	! AL304867 Tetraodon nigroviridis
gb_gss1:AWG68905	-	215.50	398.44	5.0e-13	560	! AWG68905 EST380981 MAGE rescue
gb_est2:BF117246	+	214.00	410.28	1.1e-13	126	! BF117246 u207a06.y1 NCI_CGAP_Ma
gb_est1:AAW16793	+	211.50	395.89	6.9e-13	337	! AW167693 xn47g09.x1 Soares_NHEK
gb_est1:AA024617	+	210.00	391.65	1.2e-12	389	! AA024617 y052f10.x1 Soares_test
gb_est1:AAW10331	+	210.00	388.97	1.7e-12	511	! AW210331 u153f09.r1 Rashbass md
gb_est2:BF143048	+	168.00	305.78	7.2e-08	765	! BF143048 601788733F1 NCI_CGAP_1
gb_est1:AA170494	+	158.00	294.50	3.1e-07	354	! AA170494 t144e11.x1 Soares_NSF
gb_est2:BG173847	+	156.00	280.23	1.9e-06	1029	! BG173847 t4422133906F1 NCI_CGAP
gb_est2:BG871485	+	154.00	279.45	2.1e-06	759	! BG871485 602789902F1 NCI_CGAP_5
gb_est1:AA488780	+	152.50	283.96	1.2e-06	360	! AA488780 aa34c10.r1 NCI_CGAP_GC
gb_est1:AA582560	+	146.00	277.88	2.6e-06	192	! AA582560 RCI_S70278-08010-011-
gb_est1:BE289243	+	135.00	245.15	0.0002	645	! BE289243 601092806F1 NCI_CGAP_M
gb_est1:BE2937452	+	116.50	224.34	0.0025	159	! BE2937452 RCI_S70278-310800-019-
gb_est2:BF134430	+	113.00	205.59	0.0275	533	! BF144340 372787 MARC 2P1G Sus
gb_est2:BF551964	+	110.50	202.01	0.0435	475	! BF551964 UT-R-C2p-oc-g-09-0-U1-
gb_est2:BE844365	+	108.50	193.83	0.1242	744	! BE844375 EST19 Apis mellifera
gb_est2:BE840810	+	108.00	192.76	0.0750	453	! BG080810 QVA-GN0314-281100-607-
gb_est2:BG387377	+	108.00	192.96	0.1388	738	! BG387377 602456142F1 NIH_MGC_15

```

|||||
373 CTGGTTAAACGCTGGTGGGAACCTGCTGTGTCTCCACAATTCGCAA 422
|||||
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluVal 84
|||||
423 TGAATGTCATGTGTCACCAAGCAAGTACTAAAAAATACACAGAGTCC 472
|||||
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
473 TTCAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCACATCACC 522
|||||
101 AspValAlaLeuGluHisGluCysAspCysValCysArgGlySe 117
|||||
523 GACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAG 572
|||||
117 rThrGlyGly 120
|||||
573 CACAGGAGGA 582

```

seq_name: gb_est2:BG185961

seq_documentation_block: 811 bp mRNA EST 21-APR-2001
LOCUS BG185961
DEFINITION RST4916 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG185961
VERSION BG185961.1 GI:13707648
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 811)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
Veloso,N., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J.
and Ducar,M.

TITLE Creation of Genome-wide Protein Expression Libraries using Random

Activation of Gene Expression

JOURNAL Nat. Biotechnol. 19 (5), 440 (2001) In press

COMMENT Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scaine@atersys.com

High quality sequence stop: 485.

Location/Qualifiers

1. .811

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Athersys RAGE Library"

/cell_line="H1080"

/note="See 'Creation of Genome-wide protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT 225 a 172 c 195 g 216 t 3 others

ORIGIN

alignment_scores:

Quality: 652.00 Length: 120

Ratio: 5.525 Gaps: 0

Percent Similarity: 98.333 Percent Identity: 98.333

alignment_block:

US-09-457-066-2_COPY_226_345 x BG185961 ..

Align seg 1/1 to: BG185961 from: 1 to: 811

```

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
367 GCITTTTGTGTTTGAAGAAAAATCCAGAGTGGTGGATCTGAACCTTCTAAC 416
|||||
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||
417 AGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTTCAGTGTCCA 466
|||||
34 leArgGluGluLeuLysArgThrAspThrIlePheTTPProGlyCysLeu 50
|||||
467 TAAGGGAAGAACTAAAGAAACCCATACCATTTTCTGCCAGGTTGTCTC 516
|||||
51 LeuValLysArgCysGlyArgAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
517 CTGTTTAAACGCTGTGCTGGGAACCTGTGCCTGTGTCTCCACAATTCGAA 566
|||||
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluVal 84
|||||
567 TGAATGTCAATGTGTCCCAAGCANAGTTACTAAAAAATACCAACAGGTCC 616
|||||
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
617 TTCAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCACATCACC 666
|||||
101 AspValAlaLeuGluHisGluGluCysAspCysValCysArgGlySe 117
|||||
667 GACGTGGCCCTGGAGCACCATGAGAGCTGTGACTGTGTGTCAGAGGGAG 716
|||||
117 rThrGlyGly 120
|||||
717 CACAAGAGGA 726

```

seq_name: gb_est2:BF021679

seq_documentation_block:

LOCUS BF021679

DEFINITION uy50f05.y1 NCI-CGAP.Lu30 Mus musculus cDNA clone IMAGE:3663009 5'

similar to TR:Q9QY71 Q9QY71 FALLOLEIN.; mRNA sequence.

ACCESSION BF021679.

VERSION BF021679.1 GI:10753011

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 523)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

MGI:1423777

Seq primer: -40RP from Gibco

High quality sequence stop: 452.

Location/Qualifiers

1. .523

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:3663009"

/clone_lib="NCI-CGAP.Lu30"

/tissue_type="tumor, metastatic to mammary"

/lab_host="DH10B"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH

BASE COUNT 143 a 116 c 139 g 125 t
ORIGIN

alignment_scores:
Quality: 624.00 Length: 120
Ratio: 5.288 Gaps: 0
Percent Similarity: 98.333 Percent Identity: 90.833

alignment_block:
US-09-457-066-2_COPY_226_345 x BF021679 ..
Align seg 1/1 to: BF021679 from: 1 to: 523

```
1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
164 GCTTCTGCTATGGGAAAAAAGCAAGTGGTGAATCTGAATCTCCTAAA 213

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheserValSerI 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
214 GGAAGAGGTAAACTCTACAGCTGCACACCCCGGAACCTCTCAGTGTCCA 263

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
264 TAGCGGAGAGCTTAAGAGGACAGATACCATATCTGCGCAGGTGTCTC 313

51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
314 CTGCTCAAGCGCTGTGGAGGAATTTGCTGTGTCCTCCATAATTGCAA 363

67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
364 TGAATGTCAGTGTCTCCACCGTAAGATTACAAAAAGTACCATGAGTCC 413

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
414 TTCAATGTAGACCAAAACCTGGAGTCAAGGATTCATTAAGTCACTACT 463

101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
464 GATGTGCTCTGGAACACCCAGCAGGAATGTGACTGTGTGTGAGAGGAA 513

117 rThrGlyGly 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
514 CGCAGGAGGG 523
```

seq_name: gb_est2:BE958470

seq_documentation_block:
LOCUS BE958470 523 bp mRNA EST 04-OCT-2000
DEFINITION 601644787F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930045 5',
mRNA sequence.

ACCESSION BE958470
VERSION BE958470.1 GI:10569175
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 523)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM763 row: m column: 22
High quality sequence start: 2
High quality sequence stop: 513.
Location/Qualifiers

1..523
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3930045"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pDNK-LfB (Clontech); Site_1: SfiI (ggccattggcc); Site_2: SfiI (ggccattggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT 147 a 118 c 129 g 128 t 1 others
ORIGIN

alignment_scores:
Quality: 620.00 Length: 120
Ratio: 5.254 Gaps: 0
Percent Similarity: 98.333 Percent Identity: 98.333

alignment_block:
US-09-457-066-2_COPY_226_345 x BE958470 ..

Align seg 1/1 to: BE958470 from: 1 to: 523

```
1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 GCTTCTGCTTTTCGGAAGAAATCCAGATGGTGAATCTGAACCTCTTAA 200

17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheserValSerI 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 AGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCA 250

34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 TAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTGTCTC 300

51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 CTGTTTAAACGCTGTGGTGGAACTGTGCTGTGTTCTCCACAATTGCAA 350

67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluValL 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 TGAATGTCATGTGTCCTCCCAAGCAAGTTACTAAAAAATACCAGAGGTCC 400

84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
401 TTCAGTTGAGACCAAGACCGGTGTTCAGGGGATTCACAAATCACTCACC 450

101 AspValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySe 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
451 GACGTGGC.CTGGAGCACCATGAGGAGTGTGACTGTGTGTGTGAGAGGG 499

117 rThrGlyGly 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
500 CACAGGAGGA 509
```

seq_name: gb_est2:BG609411

```

seq_documentation_block: 556 bp mRNA EST 17-APR-2001
LOCUS BG609411
DEFINITION 323251 MARC 1PTG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BG609411
VERSION BG609411.1 GI:13659390
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 556)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keeler,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACCTATGACCAT
BACKWARD: GTTTCACGTCAGCAGC
Plate: 98 row: P column: 8
Seq primer: ATTATGTCACACTATAG.
FEATURES
Location/Qualifiers
source 1..556
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PTG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 139 a 153 c 141 g 123 t
ORIGIN
alignment_scores:
Quality: 620.00 Length: 114
Ratio: 5.487 Gaps: 0
Percent Similarity: 99.123 Percent Identity: 97.368
alignment_block:
US-09-457-066-2_COPY_226_345 x BG609411 ..
Align seg 1/1 to: BG609411 from: 1 to: 556
1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
215 GCYTTTGTTCGGAAGAAATCCAGAGTGGTGATCTGAACCTTCTCAA 264
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerI 34
|||||
265 AGAAGAGTGGAGCTATACAGTCGACCCCTAGGAACCTTTTCAGTGCTA 314
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||
315 TCAGGGAAGAGCTGAAGAGAACACACACCATCTTCTGCCAGGCTGCCTC 364
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
365 CTCGTCAAGCGTTGTGGGGGAACGTGCGCTGCTGCATGCACACTGCAA 414
67 nGluCysGlnCysValProSerLysValThrLysLysThrHisGluValL 84
|||||

```

```

415 TGAGTGTCACTGTGTGTCCTCCAGCAAGTCCACCAAGAAATATCACAGGTCC 464
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
465 TTCAGTTGAGACCCACACAGAGGTGTCGGGGGGCTGCACAGTCCCTCACC 514
101 AspValAlaLeuGluHisHisGluGluCysAspCysValCys 114
|||||
515 GACGTGGCCCTGGAGCACCACGAGGAGGTGTGACTGCGGTGTGC 556
seq_name: gb_est2:BG677432
seq_documentation_block:
LOCUS BG677432 969 bp mRNA EST 01-MAY-2001
DEFINITION 602625259F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750095 5',
mRNA sequence.
ACCESSION BG677432
VERSION BG677432.1 GI:13908829
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10604 row: f column: 16
High quality sequence stop: 764.
Location/Qualifiers
source 1..969
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4750095"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 257 a 223 c 221 g 268 t
ORIGIN
alignment_scores:
Quality: 617.00 Length: 111
Ratio: 5.559 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.099
alignment_block:
US-09-457-066-2_COPY_226_345 x BG677432 ..
Align seg 1/1 to: BG677432 from: 1 to: 969
10 ValValAspLeuAsnLeuLeuThrGluGluValArgLeuTyrSerCysTh 26
|||||
4 GTGGTGGATCTGAACCTTCTAACAGAGAGGAGTAAGATTATACAGTGCAC 53
26 rProArgAsnPheSerValSerIleArgGluGluLeuLysArgThrAspT 43
|||||
54 ACCTCGTAACCTTCTCAGCGTCCATAGGGAAGAACTAAAGAGAACCGATA 103
43 hrIlePheTrpProGlyCysLeuLeuValLysArgCysGlyGlyAsnCys 59
|||||

```

```

|||||
104 CCATTTCCTGCCAGGTGTCTCTCGTTAAACGCTGTGGGGAACGTGT 153
|||||
60 AlAcysCysLeuHisAsnGluCysGlnCysValProSerLysVa 76
|||||
154 GCCTGTTGCTCCCACTTCAATGAATGTCAATGTGCCCAAGCAAGT 203
|||||
76 lThrLysLysThrHisGluValLeuGlnLeuArgProLysThrGlyVala 93
|||||
204 TACTAAAAATACCACGAGGTCCTTCACTTGAGACCAAGACCGGTGCA 253
|||||
93 rgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisGluGlu 109
|||||
254 GGGGATTGCAAAATCACTACCGACGTGGCCCTGGAGCACCATGAGGAG 303
|||||
110 CysAspCysValCysArgGlySerThrGlyGly 120
|||||
304 TGTGACTGTGTGTCAGAGGACACAGGAGGA 336
|||||

```

seq_name: gb_est2:BF151355

seq_documentation_block: 564 bp mRNA EST 29-DEC-2000
LOCUS BF151355
DEFINITION uz15b12.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3669119 5' similar to TR:09QX71 09QX71 FALLOTEIN. ; mRNA sequence.
ACCESSION BF151355
VERSION BF151355.1 GI:11032750
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 564)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
JOURNAL Tumor Gene Index
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml

MGI:1429887
Seq primer: -40RP from Gibco
High quality sequence stop: 436.
Location/Qualifiers

FEATURES
source

1..564
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:3669119"
/clone_lib="NCI-CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: Sali; Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
BASE COUNT 157 a 130 c 140 g 137 t
ORIGIN

alignment_scores:

Quality: 590.00 Length: 117
Ratio: 5.221 Gaps: 0
Percent Similarity: 96.581 Percent Identity: 88.889

alignment_block:

US-09-457-066-2_COPY_226_345 x BF151355

Align seg 1/1 to: BF151355 from: 1 to: 564

```

1 AlApheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
211 GCATTCTCTGTATGGGAAAAAGCAAGTGGTGAATCTGAATCTCCCTCAA 260
|||||
17 rGluGluValArgLeuTySerCysThrProArgAsnPheserValSerI 34
|||||
261 GGAAGAGGTAAACTCTACAGCTGCACACCCCGGAACCTCTCAGTGTCCA 310
|||||
34 leArgGluGluLeuLysArgThrAspThrIlePheTppProGlyCysLeu 50
|||||
311 TACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGCCAGGTTGTCTC 360
|||||
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
361 CTGGTCAAGCGCTGTGGAGGAAATTTGCGCTGTGTCTCCATAATTGCAA 410
|||||
67 nGluCysGlnCysValProSerLysValThrLysLysLysTyHisGluVal 84
|||||
411 TGAATGTCAGTGTCTCCCGTAAAGTTACAAAAAGTACCATGAGGTCC 460
|||||
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
461 TTCAGTTGAGACCAAAACATGGAGTCAAGGATTCATTAAGTACTCAAT 510
|||||
101 AspValAlaLeuGluHisGluGluCysAspCysValCysArgGlySe 117
|||||
511 GATGTGGCTCTTCAACACCACGAGGAATGTGACTGGGTGTGTAGAGGGAA 560
|||||
117 r 117
561 C 561

```

seq_name: gb_est1:AL047637

seq_documentation_block:

LOCUS AL047637 304 bp mRNA EST 01-MAR-2000
DEFINITION DKFZp586J042L_r1 586 (synonym: hutel) Homo sapiens cDNA clone DKFZp586J042L, mRNA sequence.
ACCESSION AL047637
VERSION AL047637.1 GI:4728633
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 304)
Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Ottenwaelder, et al.)
Unpublished (1999)
Contact: Ottenwaelder B
MIPS

REFERENCE
AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..304

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="DKFZp586J042L"

alignment_scores:

Quality: 590.00 Length: 117

Ratio: 5.221 Gaps: 0

Percent Similarity: 96.581 Percent Identity: 88.889

BASE COUNT 157 a 130 c 140 g 137 t

ORIGIN

1..304

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="DKFZp586J042L"

alignment_scores:

Quality: 590.00 Length: 117

Ratio: 5.221 Gaps: 0

Percent Similarity: 96.581 Percent Identity: 88.889

BASE COUNT 157 a 130 c 140 g 137 t

ORIGIN

1..304

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="DKFZp586J042L"

/clone_lib="586 (synonym: hutel)"
 /tissue_type="uterus"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MLuI"
 BASE COUNT 86 a 68 c 80 g 70 t
 ORIGIN

alignment_scores:
 Quality: 568.00 Length: 101
 Ratio: 5.624 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.010

alignment_block:
 US-09-457-066-2_COPY_226_345 x AL047637

Align seg 1/1 to: AL047637 from: 1 to: 304

```

18 GluGluValArgLeuTyrSerCysThrProArgAsnPheserValSerI1 34
|||||
2 GAGGAGGTAAAGTATACAGCTGCACACTCGTAACCTCTCAGTGCCAT 51
|||||
34 eArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuL 51
|||||
52 AAGGGAAGAACTAAAGAGACCGATACCATTTCTGGCCAGGTGTCTCC 101
|||||
51 euValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsn 67
|||||
102 TGGTTAAACGGCTGTGGTGGGAACCTGTGCTGTCTCCACAATTGCAAT 151
|||||
68 GluCysGlnCysValProSerLysValThrLysLysTyrHisGluValLe 84
|||||
152 GAATGTCATGTGTCCCAAGCAAGTTACTAAAAATACCCAGGTCTCT 201
|||||
84 uGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThra 101
|||||
202 TCAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCACTACCG 251
|||||
101 spValAlaLeuGluHisGluGluCysAspCysValCysArgGlySer 117
|||||
252 ACGTGGCCCTGGAGCACCATGAGGAGTGTGCTGTGTGCAGAGGGAGC 301
|||||
118 Thr 118
...
302 TCA 304

```

seq_name: gb_est2:BG243001

seq_documentation_block:
 LOCUS BG243001 910 bp mRNA EST 13-FEB-2001
 DEFINITION 602355974F1 NCI_CGAP_MamI Mus musculus cDNA clone IMAGE:4483938 5',
 mRNA sequence.

ACCESSION BG243001
 VERSION BG243001.1 GI:12752725

KEYWORDS EST.
 SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NIH-MGC <http://mgc.nci.nih.gov/>.

REFERENCE National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: Gilbert Smith, Ph.D.

cDNA library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LLAM10323 row: d column: 19
 High quality sequence stop: 690.
 Location/Qualifiers
 1. .910
 source

/organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4483938"
 /clone_lib="NCI_CGAP_MamI"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="3 months, virgin"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

BASE COUNT 242 a 220 c 250 g 198 t
 ORIGIN

alignment_scores:
 Quality: 566.00 Length: 120
 Ratio: 4.838 Gaps: 0
 Percent Similarity: 97.500 Percent Identity: 90.000

alignment_block:

US-09-457-066-2_COPY_226_345 x BG243001

Align seg 1/1 to: BG243001 from: 1 to: 910

```

1 AlaPheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
155 GCCTTCTCTATGGGAAAAAAGCAAGTGTGAATCTGAATCTCCCA 204
|||||
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheserValSerI 34
|||||
205 GGAAGAGGTAAACTCTACAGCTGCACACCCCGAACTTCTCAGTGTCCA 254
|||||
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||
255 TACGGGAAGAGCTAAAGAGACAGATACCATATTCTGGCCAGGTGTCTC 304
|||||
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysas 67
|||||
305 CTGCTCAAGCGCTGTGGAGAAA..TGTGCTGTGTCTCCATTAATGCCA 353
|||||
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluVal 84
|||||
354 TGAATGTCAGTGTGCCCGTAAAGTTACAAAAAGTACCATCAGGTCC 403
|||||
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThr 100
|||||
404 TTCAGTTGAGACCAAAACTGA..GTCAAGGGATTGCATAAGTCACTCACT 452
|||||
101 AspValAlaLeuGluHisGluGluCysAspCysValCysArgGlySe 117
|||||
453 GATGTGGCTCTGGAAACACCACGAGGAATGTGCTGTGTGTAGAGGAAA 502
|||||
117 rThrGlyGly 120
...
503 CGCAGGAGGG 512

```

seq_name: gb_est2:BF102859

seq_documentation_block:

LOCUS BF102859 851 bp mRNA EST 19-OCT-2000
 DEFINITION 601646827F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4073095 5',
 mRNA sequence.

ACCESSION BF102859

VERSION BF102859.1 GI:10885385

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens


```

3 ACACCTCGTAACCTCTCAGTGTCCATAAGGAGAACTAAAGAGAACCGA 52
42 pThrIlePheTrpProGlyCysLeuLeuValLysArgCysGlyGlyAsnC 59
|||||
53 TACCATTTCGTGGCAGGTTGTCTCTGTTAAACGCTGTGGTGGAACT 102
|||||
59 ysaLaCysCysLeuHisAsnCysAsnGluCysGlnCysValProSerLys 75
|||||
103 GTGCCTGTGCTCTCCACAATGCAATGCAATGTCATGTCCTCCAAAGCAA 152
|||||
76 ValThrLysLysTyrHisGluValLeuGlnLeuArgProLysThrGlyVa 92
|||||
153 GTTACTAAAAAATACCAGAGGCTCTTCAGTTGAGACCAAGACCGGTCT 202
|||||
92 lArgGlyLeuHisLysSerLeuThrAspValAlaLeuGluHisGluG 109
|||||
203 CAGGGATTGCACAATACATCCAGGAGTGGCCCTGGAGCACAATAGAGG 252
|||||
109 lCysAspCysValCysArgGlySerThrGlyGly 120
|||||
253 AGTGTGACTGTGTGCAGAGGGAGCACAGGAGGA 287
|||||

seq_name: gb_est2:BF011835

seq_documentation_block:
LOCUS BF011835 447 bp mRNA EST 06-OCT-2000
DEFINITION us37d10.y1.Soares_NMEBA_branchial_arch.Mus musculus cDNA clone
IMAGE:3169267 5' similar to TR:09Q171.Q9Q171.FALL0TEIN.;, mRNA
sequence.
ACCESSION BF011835
VERSION BF011835.1 GI:10712110
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1064727
Seq primer: -40RP from Gibco
High quality sequence stop: 402.
Location/Qualifiers
1. 447
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3169267"
/clone_lib="Soares_NMEBA_branchial_arch"
/tissue_type="branchial arches"
/dev_stage="embryo, 10.5 dpc"
/lab_host="DH10B (phage resistant)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCATGTCATTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT 126 a 104 c 108 g 109 t

```

```

ORIGIN
alignment_scores:
Quality: 514.00 Length: 100
Ratio: 5.245 Gaps: 0
Percent Similarity: 98.000 Percent Identity: 91.000
alignment_block:
US-09-457-066-2_COPY_226_345 x BF011835
Align seg 1/1 to: BF011835 from: 1 to: 447
1 AlapheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuTh 17
|||||
148 GCITTCCTGTATGGGAAAAAACAAGTGGTGAATCTGAATCTCCTCAA 197
|||||
17 rGluGluValArgLeuTyrSerCysThrProArgAsnPheSerValserI 34
|||||
198 GGAAGAGGTAAAACTCTACAGCTGCACACCCCGAACTTCTCAGTGTCCA 247
|||||
34 leArgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeu 50
|||||
248 TACGGGAGAGGCTAAAGAGGACAGATACCATATTTCTGGCAGGTTGTCTC 297
|||||
51 LeuValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAs 67
|||||
298 CTGCTCAAGCGCTGTGGAGAAATGTGCTGTGTCTCCATAATGTGCAA 347
|||||
67 nGluCysGlnCysValProSerLysValThrLysLysTyrHisGluVal 84
|||||
348 TGAATGTCAGTGTGTCCTCCAGTAAAGTTACAAAAAGTACCATGAGGTCC 397
|||||
84 euGlnLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuTh 100
|||||
398 TTCAGTTGAGACCAAAACATGGAGTCAAGGATTGCATAAATCACTCACT 447
|||||

seq_name: gb_est2:BF670092

seq_documentation_block:
LOCUS BF670092 874 bp mRNA EST 21-DEC-2000
DEFINITION 602119417F1.NIH_MGC_56.Homo sapiens cDNA clone IMAGE:4276493 5',
mRNA sequence.
ACCESSION BF670092
VERSION BF670092.1 GI:11943987
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 874)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1097 row: a column: 06
High quality sequence stop: 598.
Location/Qualifiers
1. 874
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4276493"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"

```


/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccctggcc); Site_2: Sfil (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGCCACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 227 a 208 c 245 g 194 t
ORIGIN

alignment_scores:
Quality: 463.00 Length: 122
Ratio: 4.287 Gaps: 8
Percent Similarity: 88.525 Percent Identity: 86.885

alignment_block:
US-09-457-066-2_COPY_226_345 x BF670092

Align seg 1/1 to: BF670092 from: 1 to: 874

5 GlyArgLysSerArgValValAspLeuAsnLeuLeuThrGluGluVal 21
|||||
77 GGAAGAAATCCAGAGTGGTGATCTGAACCTTCTAACAGAGGAGTAAG 126

21 gLeu..TyrSerCysThrProArgAsnPheSerValSerIleArg.GluG 37
|||||
127 ATTATAGCATGCTGCACACCTCGTAACCTTCTCAGTGTCCATAATGGGAAG 176

37 LuLeuLysArgThrAspThrIle.PheTrpProGlyCysLeuLeuVal 53
|||||
177 AACTAAAGAACCGATGACCAATGTTCTGGCCAGGTTCTCTCCCTGGTTAA 226

53 sArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsnGluCysG 70
|||||
227 AGCGTGTGGTGGGAACGTGCTGCTGCTCCACAAATTCGAATGATGTC 276

70 In.CysValProSerLysValThrLysLysThrHis.GluValLeuInL 86
|||||
277 AAGTGTGTCCCAAGCAAGTGTACTTAAAAAATACCAGCGAGGTCCCTCAGT 326

86 euArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAspVal 102
|||||
327 TGAGACCAAGACCGGTGTACGGGGATGGTCACAAATCACTCACCAGCAGTG 376

103 AlaLeuGluHis.HisGlu.GluCysAspCys.ValCysArgGlySerTh 118
|||||
377 GCCCTGAGCAGCATGAGAGTGTGACTGCTGCTGTCAGAGGGAGGCAC 426

118 r 118
|

427 A 427

seq_name: gb_est2:BG118707

seq_documentation_block:
LOCUS BG118707 968 bp mRNA EST 30-JAN-2001
DEFINITION 602348280F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4443498 5',
mRNA sequence.

ACCESSION BG118707

VERSION BG118707.1 GI:12612213

KEYWORDS EST.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 968)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1AM10217 row: o column: 19
High quality sequence start: 8
High quality sequence stop: 574.
Location/Qualifiers

FEATURES

source

1. 968
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4443498"
/clone_lib="NIH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 313 a 230 c 219 g 206 t
ORIGIN

alignment_scores:
Quality: 442.00 Length: 119
Ratio: 4.857 Gaps: 1
Percent Similarity: 76.471 Percent Identity: 76.471

alignment_block:

US-09-457-066-2_COPY_226_345 x BG118707

Align seg 1/1 to: BG118707 from: 1 to: 968

2 PheValPheGlyArgLysSerArgValValAspLeuAsnLeuLeuThrG 18
|||||
224 TTTGTTTTTGGAGAAATCCAGAGTGGTGATCTGAACCTTCTAACAGA 273

18 uGluValArgLeuTyrSerCysThrProArgAsnPheSerValSerIle 35
|
274 GGA..... 276

35 rgGluGluLeuLysArgThrAspThrIlePheTrpProGlyCysLeuLe 51
|||||
277GGTTGCTCTCTG 288

52 ValLysArgCysGlyGlyAsnCysAlaCysCysLeuHisAsnCysAsn 68
|||||
289 GTTAAACGCTGTGGTGGAACTGTGCTGTGTCTCCACAATTCGAATGA 338

68 uCysGlnCysValProSerLysValThrLysLysTyrHisGluValLeu 85
|||||
339 ATGTCAATGTGTCACCAAGCAAGTTACTAAAAAATACCACGAGGTCCTTC 388

85 InLeuArgProLysThrGlyValArgGlyLeuHisLysSerLeuThrAs 101
|||||
389 AGTTGAGACCAAGACCGGTGTGAGGGGATTCACAAATCACTCCACCGAC 438

102 ValAlaLeuGluHisHisGluGluCysAspCysValCysArgGlySerTh 118
|||
439 GTGGC.CTGGAGCACCATGAGGAGTGTGCTGTGTGTCAGAGGGAGCAC 487

118 rGlyGly 120
|||||

488 AGGAGGA 494

seq_name: gb_gss:CNS024MX

